

111023

**Ruhl, Mary Jane**

**From:** Schnizer, Holly  
**Sent:** Monday, December 29, 2003 10:29 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** seq. search for appl. no. 09/809,827

*emp# 76558*

Please search all databases (inc. interference) for SEQ ID NO: 31 and rev. translation of SEQ ID NO:31.

Thank you.

Holly Schnizer  
AU 1653  
CM1-9E09  
305-3722  
mailbox: CM1-9B01

*PLEASE SCAN  
SUMMARY of SEARCH*

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:51:25 ; Search time 17 Seconds  
(without alignments)  
821.584 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHAWSLKDLGAVAAA.....LRGMGAFVLVLYDEIKYV 297

Scoring table: BLOSUM62

Gapop 10.0., Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526.5	98.3	298	1	ADT1_HUMAN
2	1466.5	94.4	298	1	ADT1_RAT
3	1463.5	94.2	298	1	ADT1_MOUSE
4	1453.5	93.6	297	1	ADT1_BOVIN
5	1408.5	90.7	298	1	ADT2_MOUSE
6	1407.5	90.6	298	1	ADT2_RAT
7	1398.5	90.1	298	1	ADT2_HUMAN
8	1385.5	89.2	298	1	ADT3_HUMAN
9	1380.5	88.9	298	1	ADT3_BOVIN
10	1241	79.9	299	1	ADT1_DROME
11	1162.5	74.9	301	1	ADT1_ANOGA
12	973.5	62.7	339	1	ADT1_CHLKE
13	770.5	49.6	308	1	ADT1_CHLRE
14	756.5	48.7	387	1	ADT1_MAIZE
15	752.5	48.5	322	1	ADT1_SCHPO
16	752.5	48.5	386	1	ADT1_GOSHI
17	751.5	48.4	382	1	ADT1_ORYZA
18	751.5	48.4	387	1	ADT2_MAIZE
19	746	48.0	381	1	ADT1_ARATH
20	744.5	47.9	386	1	ADT1_SOLTU
21	742.5	47.8	331	1	ADT1_WHEAT
22	740	47.6	386	1	ADT2_SOLTU
23	736	47.4	307	1	ADT3_YEAST
24	734	47.3	318	1	ADT2_YEAST
25	733.5	47.2	313	1	ADT1_NEUCR
26	731	47.1	385	1	ADT2_ARATH
27	729	46.9	305	1	ADT1_KLULA
28	728.5	46.9	331	1	ADT2_WHEAT
29	716.5	46.3	309	1	ADT1_YEAST
30	702.5	19.5	678	1	CNC1_HUMAN
31	309.5	19.3	330	1	GDC_BOVIN
32	296.5	19.1	565	1	CNC3_CABEL
33	296.5	19.1	702	1	CNC1_CABEL

## RESULT 1

ID	ADT1_HUMAN	STANDARD;	PRT;	298 AA.
AC	P12235;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).			
GN	SLC25A4 OR ANT1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89236396; PubMed=2541251;			
RA	Cozens A.L., Runswick M.J., Walker J.E.;			
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";			
RL	J. Mol. Biol. 206:261-280 (1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89340499; PubMed=2547778;			
RA	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;			
RT	"A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed.";			
RL	J. Biol. Chem. 264:13998-14004 (1989).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88041149; PubMed=2823266;			
RA	Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;			
RT	"cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584 (1987).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Hailton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

34	296	19.1	588	1	CMC2_CABEL	Q20799 caenorhabdi
35	295	19.0	322	1	GDC_RAT	P16261 rattus norv
36	292.5	18.8	307	1	ODC3_YEAST	Q99297 saccharomyc
37	292	18.7	332	1	GDC_HUMAN	P16260 homo sapien
38	291	18.7	675	1	CMC2_HUMAN	Q9h2d1 homo sapien
39	280	18.0	315	1	MPT_HUMAN	Q9h2d1 homo sapien
40	279.5	18.0	676	1	CMC3_MOUSE	Q9qxx4 mus musculu
41	270.5	17.4	315	1	SA18_HUMAN	Q9h1k4 homo sapien
42	267.5	17.2	325	1	UCP5_MOUSE	Q9z2b2 mus musculu
43	266.5	17.2	310	1	ODC3_YEAST	Q03028 saccharomyc
44	265.5	17.1	325	1	UCP5_HUMAN	Q95258 homo sapien
45	263.5	17.0	695	1	CMC1_DROME	Q9va73 drosophila

## ALIGNMENTS

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RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[5]  
RP SEQUENCE OF 1-37 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=88124845; PubMed=2829183;  
RA Houldsworth J., Attardi G.;  
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
level in adult human liver.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
[6]  
RN VARIANTS: PEO PRO-114 AND MET-289.  
RP MEDLINE=20385067; PubMed=10926541;  
RX Kaukonen J., Juselius J.K., Tiranti V., Kytälä A., Zeviani M.,  
RA Comi G.P., Keranen J., Peltonen L., Suomalainen A.;  
RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";  
RL Science 289:782-785(2000).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant  
progressive external ophthalmoplegia with various mitochondrial  
DNA deletions (PEO). Patients with PEO have mitochondrial  
myopathy, progressive external ophthalmoplegia, and other  
abnormalities associated with multiple different deletions of  
mitochondrial DNA.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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EMBL; J02966; AAA61223.1; -;  
EMBL; J03593; AAA36751.1; -;  
EMBL; J04982; AAA51736.1; -;  
EMBL; BC008664; AAA08664.1; -;  
PIR; A44778; A44778.  
Genew; HGNC:10990; SLC25A4.  
MIM; 103220; -;  
MIM; 157640; -;  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0005739; C:mitochondrion; TAS.  
DR GO; GO:0015207; F:adenine transporter activity; TAS.  
DR GO; GO:0006091; P:energy pathways; TAS.  
DR GO; GO:0000002; P:mitochondrial genome maintenance; TAS.  
DR GO; GO:0006832; P:small molecule transport; TAS.  
InterPro; IPR002067; Mit. carrier.  
InterPro; IPR002030; Mit. uncoupling.  
InterPro; IPR001993; Mitoch. carrier.  
Pfam; PF00153; mito. carr.; 3.  
PRINTS; PR00926; MITOCARRIER.  
PRINTS; PR00784; MTUNCOUPLING.  
PROSITE; PS00215; MITOCH. CARRIER; 3.  
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
multigene family; Disease mutation.  
TRANSMEM 12 29  
TRANSMEM 73 91  
TRANSMEM 117 134  
TRANSMEM 176 195  
TRANSMEM 214 231  
TRANSMEM 273 291  
TRANSMEM 1 110  
TRANSMEM 111 208

FT REPEAT 209 298 3.  
FT VARIANT 114 114 A -> P (IN PEO).  
FT FTIG=VAR 012111.  
FT V -> M (IN PEO).  
FT VARIANT 289 289 /FTIG=VAR 012112.  
FT G -> A (IN REF. 3).  
FT CONFLICT 16 16 KGA -> RR (IN REF. 3).  
FT CONFLICT 147 149 V -> L (IN REF. 3).  
FT CONFLICT 227 227 V -> L (IN REF. 3).  
SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAEC4E7CFBB CRC64;  
Query Match 98.3%; Score 1526.5; DB 1; Length 298;  
Best Local Similarity 98.3%; Pred. No. 28-129;  
Matches 293; Conservative 2; Mismatches 1; Gaps 1;  
QY 1 MGDHAWSLKDFLAGAAVAASKTAVAPIERVKLLLOVHASKQISAEQYKGIIDCVVR 60  
DB 1 MGDHAWSLKDFLAGAAVAASKTAVAPIERVKLLLOVHASKQISAEQYKGIIDCVVR 60  
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFGLGVDRHKQFWRYPAGNLSG 120  
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFGLGVDRHKQFWRYPAGNLSG 120  
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180  
QY 180 VQIIIIYRAAYFGVDTAKGMLPDPKQNVHIFVSWIAQSVTAVAGLLSVFDTVRRMM 239  
DB 181 VQIIIIYRAAYFGVDTAKGMLPDPKQNVHIFVSWIAQSVTAVAGLLSVFDTVRRMM 240  
QY 240 QSGRKGADIMYTGTVDCWRKIAKDEKAGAFFKGANVNLGRMGAPVLVLYDEIKKYV 297  
DB 241 QSGRKGADIMYTGTVDCWRKIAKDEKAGAFFKGANVNLGRMGAPVLVLYDEIKKYV 298  
RESULT 2  
ADTI RAT  
ID ADT1 RAT STANDARD; PRT; 298 AA.  
AC Q05922;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE ADP.ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP  
translocase 1) (Adenine nucleotide translocator 1) (ANT 1).  
GN SLC25A4 OR ANT1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RC SEQUENCE FROM N.A.  
RP STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;  
RX MEDLINE=94002161; PubMed=8399300;  
RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;  
RT "Isolation and characterization of cDNA clones and a genomic clone  
encoding rat mitochondrial adenine nucleotide translocator.";  
RL Biochim. Biophys. Acta 1152:192-196(1993).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
inner membrane.  
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER  
EXTENT, IN BRAIN AND KIDNEY.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
-----  
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Run on: December 30, 2003, 09:51:25 ; Search time 17 seconds  
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Sequence: 1 MGDHWSFLKFLAGAVAAA.....LRGMGAFVLVLYDEIKYV 297

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Total number of hits satisfying chosen parameters: 127863

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Listing first 45 summaries

Database : SwissProt\_41.\*

\*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126.5	98.3	298	1 ADT1_HUMAN	P12235 homo sapien
2	126.5	94.4	298	1 ADT1_RAT	Q05962 rattus norv
3	1463.5	94.2	298	1 ADT1_MOUSE	P48962 mus musculu
4	1453.5	93.6	297	1 ADT1_BOVIN	P02722 bos taurus
5	1408.5	90.7	298	1 ADT2_MOUSE	P51861 mus musculu
6	1407.5	90.6	298	1 ADT2_RAT	Q09073 rattus norv
7	1398.5	90.1	298	1 ADT2_HUMAN	P05141 homo sapien
8	1385.5	89.2	298	1 ADT3_HUMAN	P12236 homo sapien
9	1380.5	88.9	298	1 ADT3_BOVIN	P32007 bos taurus
10	1241.5	79.9	299	1 ADT1_DROME	*Q26365 drosophila
11	1162.5	74.9	301	1 ADT_ANGOA	*Q27238 anopheles g
12	973.5	62.7	339	1 ADT_CHLXE	P31692 chlorella k
13	770.5	49.6	308	1 ADT1_CHLRE	P27080 chlamydomon
14	756.5	48.7	387	1 ADT1_MAIZE	P04709 zea mays (m
15	752.5	48.5	322	1 ADT1_SCHPO	Q09188 schizosacch
16	752.5	48.5	386	1 ADT1_GOSHI	Q22342 gossypium h
17	751.5	48.4	382	1 ADT_ORYSA	P31691 oryza sativ
18	751.5	48.4	387	1 ADT2_MAIZE	P12857 zea mays (m
19	746	48.0	381	1 ADT1_ARATH	P31167 arabidopsis
20	744.5	47.9	386	1 ADT1_SOLTU	P25083 solanum tub
21	742.5	47.8	331	1 ADT1_WHEAT	P41629 triticum ae
22	740	47.6	386	1 ADT2_SOLTU	P27081 solanum tub
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24	734	47.3	318	1 ADT2_YEAST	P18239 saccharomyc
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26	731	47.1	385	1 ADT2_ARATH	P40941 arabidopsis
27	729	46.9	305	1 ADT_KLULA	P49382 kluyveromyc
28	728.5	46.9	331	1 ADT2_WHEAT	Q41630 triticum ae
29	718.5	46.3	309	1 ADT1_YEAST	P04710 saccharomyc
30	302.5	19.5	678	1 CMC1_HUMAN	O05746 homo sapien
31	300.5	19.3	330	1 GDC_BOVIN	Q01888-bos-taurus
32	296.5	19.1	565	1 CMC3_CAEEL	Q19529 caenorhabdi
33	296.5	19.1	702	1 CMC1_CAEEL	Q21153 caenorhabdi

RESULT 1  
ADT1\_HUMAN  
ID ADT1\_HUMAN STANDARD; PRT; 298 AA.  
AC P12235;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocator 1) (Adenine nucleotide translocator 1) (ANT 1).  
GN SLC25A4 OR ANTI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89236396; PubMed=2541251;  
RA Cozens A.L., Runswick M.J., Walker J.E.;  
RT "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";  
RL J. Mol. Biol. 206:261-280(1989).  
RN [2]  
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RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;  
RT "A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed.";  
RL J. Biol. Chem. 264:13998-14004(1989).  
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RX MEDLINE=88041149; PubMed=2823266;  
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;  
RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Eye;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.P., Bhat N.K., Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Heieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

## ALIGNMENTS

34 296 19.1 588 1 CMC2\_CAEEL Q02799 caenorhabdi  
35 295 19.0 322 1 GDC\_RAT P16261 rattus norv  
36 292.5 18.8 307 1 ODC2\_YEAST Q99297 saccharomyc  
37 292 18.8 332 1 GDC\_HUMAN P16260 homo sapien  
38 291 18.7 675 1 CMC2\_HUMAN Q9UJ80 homo sapien  
39 280 18.0 315 1 MFT\_HUMAN Q9H2D1 homo sapien  
40 279.5 18.0 676 1 CMC2\_MOUSE Q9QXX4 mus musculu  
41 270.5 17.4 315 1 SAI18\_HUMAN Q9H1K4 homo sapien  
42 267.5 17.2 325 1 UCP5\_MOUSE Q9Z2B2 mus musculu  
43 266.5 17.2 310 1 ODC1\_YEAST Q03028 saccharomyc  
44 265.5 17.1 325 1 UCP5\_HUMAN Q9S258 homo sapien  
45 263.5 17.0 695 1 CMC1\_DROME Q9VA73 drosophila

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
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 RC TISSUE=Liver;  
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 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 RT level in adult human liver.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
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 RP VARIANTS: PEO PRO-114 AND MET-289.  
 RX MEDLINE=20385067; PubMed=10926541;  
 RA Kaukonen J., Juselius J.K., Tiranti V., Kytala A., Zeviani M.,  
 RA Comi G.P., Keranen J., Peltonen L., Suomalainen A.;  
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";  
 RL Science 289:782-785(2000).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DISEASE: DEFECTS OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant  
 CC progressive external ophthalmoplegia with various mitochondrial  
 CC DNA deletions (PEO). Patients with PEO have mitochondrial  
 CC myopathy, progressive external ophthalmoplegia, and other  
 CC abnormalities associated with multiple different deletions of  
 CC mitochondrial DNA.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; J02966; AAA61223.1; -;  
 DR EMBL; J03593; AAA36751.1; -;  
 DR EMBL; J04982; AAA51735.1; -;  
 DR EMBL; BC008664; AAH08664.1; -;  
 DR PIR; A44778; A44778.  
 DR Genew; HGNC:10990; SLC25A4.  
 DR MIM; 103220; -;  
 DR MIM; 157640; -;  
 DR CO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR CO; GO:0005739; C:mitochondrion; TAS.  
 DR CO; GO:0015207; P:adenine transporter activity; TAS.  
 DR CO; GO:0006091; P:energy pathways; TAS.  
 DR CO; GO:0000002; P:mitochondrial genome maintenance; TAS.  
 DR CO; GO:0006832; P:small molecule transport; TAS.  
 DR InterPro; IPR002067; Mit carrier.  
 DR InterPro; IPR002030; Mit uncoupling.  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR Pfam; PF00153; mito carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family; Disease mutation.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 311 6 (POTENTIAL).  
 FT REPEAT 1 110 1.  
 FT REPEAT 111 208 2.

FT REPEAT 209 298 3.  
 FT VARIANT 114 114 A -> P (IN PEO).  
 FT /FTID=VAR 012111.  
 FT V -> M (IN PEO).  
 FT VARIANT 289 289 /FTID=VAR 012112.  
 FT G -> A (IN REF. 3).  
 FT CONFLICT 16 16 KGA -> RR (IN REF. 3).  
 FT CONFLICT 147 149 V -> L (IN REF. 3).  
 FT CONFLICT 227 227 V -> L (IN REF. 3).  
 SQ SEQUENCE 298 AA; 33064 MW; 59F0DFARC4E7CFBB CRC64;  
 Query Match 98.3%; Score 1526.5; DB 1; Length 298;  
 Best Local Similarity 98.3%; Pred. No. 28-129;  
 Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
 QY 1 MGDHWSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKQISAQYKGIIDCVVR 60  
 DB 1 MGDHWSFLKDFLAGGAAVSKTAVAPIERVKLLLOVHASKQISAQYKGIIDCVVR 60  
 QY 61 IPKEQGFISFWRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
 DB 61 IPKEQGFISFWRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNV 179  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNV 180  
 QY 180 VQGIIRYRAAYGVVDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSPFDTVRRMM 239  
 DB 181 VQGIIRYRAAYGVVDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSPFDTVRRMM 240  
 QY 240 QSGRGADIMYTGTVDCWRKIAKDEGAKAFPGANVLRGMGGAFVLVLYDEIKYV 297  
 DB 241 QSGRGADIMYTGTVDCWRKIAKDEGAKAFPGANVLRGMGGAFVLVLYDEIKYV 298  
 RESULT 2  
 ADT1 RAT  
 ID ADT1 RAT STANDARD; PRT; 298 AA.  
 AC Q05962;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP  
 DE translocase 1) (adenine nucleotide translocator 1) (ANT 1).  
 GN SLC25A4 OR ANT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]\_TaxID=10116;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;  
 RX MEDLINE=94002161; PubMed=8399300;  
 RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;  
 RT "Isolation and characterization of cDNA clones and a genomic clone  
 RT encoding rat mitochondrial adenine nucleotide translocator.";  
 RL Biochim. Biophys. Acta 1152:192-196(1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER  
 CC EXTENT, IN BRAIN AND KIDNEY.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC  
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; X61667; CAA43842.1; -.
CC      DR      EMBL; D12770; BAA02237.1; -.
CC      DR      PIR; I60173; I60173.
CC      DR      InterPro; IPR002067; Mit_carrier.
CC      DR      InterPro; IPR002030; Mit_uncoupling.
CC      DR      Pfam; PF00153; mito_carr; 3.
CC      DR      PRINTS; PR00926; MITOCARRIER.
CC      DR      PROSITE; PS00784; MTUNCOUPLING.
CC      DR      PROSITE; PS00215; MITOCH CARRIER; 3.
CC      KW      Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC      KW      Multigene family.
CC      FT      TRANSMEM 12 29 1 (POTENTIAL).
CC      FT      TRANSMEM 73 91 2 (POTENTIAL).
CC      FT      TRANSMEM 117 134 3 (POTENTIAL).
CC      FT      TRANSMEM 176 195 4 (POTENTIAL).
CC      FT      TRANSMEM 214 231 5 (POTENTIAL).
CC      FT      TRANSMEM 273 291 6 (POTENTIAL).
CC      FT      REPEAT 1 110 1.
CC      FT      REPEAT 111 208 2.
CC      FT      REPEAT 209 298 3.
CC      SQ      SEQUENCE 298 AA; 32989 MW; 66704FPF78C5BC320 CRC64;

Query Match          94.4%; Score 1466.5; DB 1; Length 298;
Best Local Similarity 94.3%; Pred. No. 4.7e-124;
Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY      1 MGDHANSFLKDFLAGAAVASTAVAPIRVKLLQVHQAQISAEKQYKGIICVVR 60
DB      1 MGDQALSFLKDFLAGGIAVASTAVAPIRVKLLQVHQAQISAEKQYKGIICVVR 60

QY      61 IPKEQGLSFWGRNLNVIRYFTQALNPAFKDKYKQLFLGGVDRHKQFVYFAGNLASG 120
DB      61 IPKEQGLSFWGRNLNVIRYFTQALNPAFKDKYKQLFLGGVDRHKQFVYFAGNLASG 120

QY      121 GAAGATSLCFVYPLDFARTLRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
DB      121 GAAGATSLCFVYPLDFARTLRLAADVGRKQSFQREFNGLDCLTKIFKSDGLKGLYQGFVS 180

QY      180 VQGIILYRAAYFGVYDTAKGMLPDPKRVHIFVSNIAQSVTAAGLLSYFPDFTVRRMM 239
DB      181 VQGIILYRAAYFGVYDTAKGMLPDPKRVHIFVSNIAQSVTAAGLLSYFPDFTVRRMM 240

QY      240 QSGRKADIMYTGTCVDCWRKIADDEGAKAFPKGAWSNVLRGMGGAFVLVLYDEIKYV 297
DB      241 QSGRKADIMYTGTCVDCWRKIADDEGAKAFPKGAWSNVLRGMGGAFVLVLYDEIKYV 298

RESULT 3
ADT1_MOUSE STANDARD; PRT; 298 AA.
AC      P48962; Q62164;
DT      01-FEB-1996 (Rel. 33, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DE      ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE      translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (mANCL1).
GN      SLC25A4 OR ANT1 OR ANCL1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=Brain;
RX      MEDLINE=97059403; PubMed=8903724;
RA      Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT      "Rapid evolution of human pseudoautosomal genes and their mouse
RL      homologs."
RM      Mamm. Genome 7:25-30 (1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c; TISSUE=Muscle;
RA      Laplace C., Costet P.;
RL      Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT      "Expression and sequence analysis of the mouse adenine nucleotide
RT      translocase 1 and 2 genes."
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Eye;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Lottolano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences."
RL      Proc. Natl Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC      -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC      MITOCHONDRIAL INNER MEMBRANE.
CC      -!- SUBUNIT: Homodimer.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane.
CC      -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC      -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; U27315; AAC52837.1; -.
CC      DR      EMBL; X74510; CAA52616.1; -.
CC      DR      EMBL; AF240002; AAF64470.1; -.
CC      DR      EMBL; BC003791; AAH03791.1; -.
CC      DR      EMBL; BC026925; AAH26925.1; -.
CC      DR      PIR; S37210; S37210.
CC      DR      MGD; MGI:1353495; Slc25a4.
CC      DR      InterPro; IPR002067; Mit_carrier.
CC      DR      InterPro; IPR002030; Mit_uncoupling.
CC      DR      Pfam; PF00153; mito_carr; 3.
CC      DR      PRINTS; PR00926; MITOCARRIER.
CC      DR      PRINTS; PR00784; MTUNCOUPLING.
CC      DR      PROSITE; PS00215; MITOCH CARRIER; 3.
CC      KW      Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC      KW      Multigene family.
CC      FT      TRANSMEM 12 29 1 (POTENTIAL).
CC      FT      TRANSMEM 73 91 2 (POTENTIAL).
CC      FT      TRANSMEM 117 134 3 (POTENTIAL).
CC      FT      TRANSMEM 176 195 4 (POTENTIAL).
CC      FT      TRANSMEM 214 231 5 (POTENTIAL).
CC      FT      TRANSMEM 273 291 6 (POTENTIAL).
CC      FT      REPEAT 1 110 1.

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FT REPEAT      111 208 2.
FT REPEAT      209 298 3.
FT CONFLICT    136 136 F -> L (IN REF. 1).
SQ SEQUENCE    298 AA; 32904 MW; 3A849FEAB0961462 CRC64;

Query Match      94.2%; Score 1463.5; DB 1; Length 298;
Best Local Similarity 94.0%; Pred. No. 8.7e-124;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAATAVAPISVKTAVPIRVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDQALSFLKDFLAGGTAATAVAPISVKTAVPIRVKLLQVHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGLSWRGNLANVIRVFPTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASG 120
DB 61 IPKEQGLSWRGNLANVIRVFPTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
QY 180 VQGIIRYRAAYFGYDITAKGMLPDPKPNVHIIVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
DB 181 VQGIIRYRAAYFGYDITAKGMLPDPKPNVHIIVSWMIAQSVTAVAGLLSYFPDTRRRMM 240
QY 240 QSGRKGADIMYTGTCWCRKIADEGAKAFKGAWSNVLKGMGAFVLVLYDEIKKYV 297
DB 241 QSGRKGADIMYTGTCWCRKIADEGAKAFKGAWSNVLKGMGAFVLVLYDEIKKYV 298

RESULT 4
ADT1_BOVIN STANDARD; PRT; 297 AA.
AC P02722;
DC 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP, ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC2A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873 (1989).
RN [2]
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Mista D., Bullitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349 (1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857 (1986).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.

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CC -----
DR EMBL; M13783; AAA30363.1; -
DR EMBL; M24102; AAA30768.1; -
DR PIR; A43646; XWBO.
DR InterPro; IPR002067; Mit carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT INIT MET 0 0
FT MOD RES 1 1 1 BLOCKED.
FT TRANS MEM 51 51 1 METHYLATION (POTENTIAL).
FT TRANS MEM 11 28 1 (POTENTIAL).
FT TRANS MEM 72 90 2 (POTENTIAL).
FT TRANS MEM 116 133 3 (POTENTIAL).
FT TRANS MEM 175 194 4 (POTENTIAL).
FT TRANS MEM 213 230 5 (POTENTIAL).
FT TRANS MEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;

Query Match      93.6%; Score 1453.5; DB 1; Length 297;
Best Local Similarity 94.6%; Pred. No. 6.8e-123;
Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 3 DHAMSLKDFLAGAATAVAPISVKTAVPIRVKLLQVHASKQISAEKQYKGIIDCVVRIP 62
DB 2 DQALSFLKDFLAGGTAATAVAPISVKTAVPIRVKLLQVHASKQISAEKQYKGIIDCVVRIP 61
QY 63 KEQGLSWRGNLANVIRVFPTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASGA 122
DB 62 KEQGLSWRGNLANVIRVFPTQALNFAKDKYKQIFLGVDVDRHKQFWRYPAGNLASGA 121
QY 123 AGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSQ 181
DB 122 AGATSLCFVYPLDFARTLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSQ 181
QY 182 GIIIRYRAAYFGYDITAKGMLPDPKPNVHIIVSWMIAQSVTAVAGLLSYFPDTRRRMMQ 241
DB 182 GIIIRYRAAYFGYDITAKGMLPDPKPNVHIIVSWMIAQSVTAVAGLLSYFPDTRRRMMQ 241
QY 242 GSKGADIMYTGTCWCRKIADEGAKAFKGAWSNVLKGMGAFVLVLYDEIKKYV 297
DB 242 GRKGADIMYTGTCWCRKIADEGAKAFKGAWSNVLKGMGAFVLVLYDEIKKYV 297

RESULT 5
ADT2_MOUSE STANDARD; PRT; 298 AA.
AC P51881; Q61311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP, ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; Tissue=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RL homologs.";
RN Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Costet P., Laplace C.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RA Laplace C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20432087; PubMed=10974536;
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RL translocase 1 and 2 genes.";
RN Gene 254:57-66(2000).
CC -f- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC -f- MITOCHONDRIAL INNER MEMBRANE.
CC -l- SUBUNIT: Homodimer.
CC -l- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -l- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -l- SIMILARITY: Belongs to the mitochondrial carrier family.
CC [1]
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CC or send an email to license@isb-sib.ch).
CC -----
DR ENBL; U27316; AAC52838.1; --
DR ENBL; U10404; AAA19009.1; --
DR ENBL; X70847; CAA50196.1; --
DR ENBL; AF240003; AAF64471.1; --
DR MGD; MGI:1353496; SLC25a5.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
FT REPEAT 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;
SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;

Query Match 90.7%; Score 1408.5; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 7.3e-119;

Matches 266; Conservative 17; Mismatches 13; Indels 1; Gaps 1;
QY 1 MGDHAWSLKDLGAVAAVSKTAVAPIERVKLLQVHQAQSAEKYKGIIDCVVR 60
DB 1 MTDAVVSFAKDFLAGGVAARIKSTAVAPIERVKLLQVHQAQSAEKYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLSG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLSG 120
QY 121 GAAGATSLCFVYPLDPARTLAADVGR--AOREPHGLGDCIIKPKSGDLGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDPARTLAADVGR--AOREPHGLGDCIIKPKSGDLGLYQGFNV 180
QY 180 VQIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSLSPFDVRRMM 239
DB 180 VQIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSLSPFDVRRMM 240
QY 240 QSGRGADIMYTGTVDCWRKIAKDEGAKAPFKGANSNVLGRMGGAFLVLYDIKKY 296
DB 241 QSGRGADIMYTGTVDCWRKIAKDEGAKAPFKGANSNVLGRMGGAFLVLYDIKKY 297

RESULT 6
ADT2_RAT
ID ADT2_RAT STANDARD; PRT; 298 AA.
AC Q09073;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; Tissue=Liver;
RX MEDLINE=9402161; PubMed=8399300;
RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RL encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -f- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC -f- MITOCHONDRIAL INNER MEMBRANE.
CC -l- SUBUNIT: Homodimer.
CC -l- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -l- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
CC SKELETAL MUSCLE.
CC -l- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -l- SIMILARITY: Belongs to the mitochondrial carrier family.
CC [1]
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CC or send an email to license@isb-sib.ch).
CC -----
DR ENBL; D12771; BAA02238.1; --
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.

```

```
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987E35 CRC64;

Query Match 90.6%; Score 1407.5; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 9e-119;
Matches 266; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 1 MGDHAWSLKDFLAGAATAVSTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Db 1 MTDAAVSPAKDFLAGGVAATAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60

QY 61 IPKEQGLSPWRGNLANVIRYFTQALNPAFKDKYKQLFLGGVDHKKQFWRYFAGNLSG 120
Db 61 IPKEQGLSPWRGNLANVIRYFTQALNPAFKDKYKQLFLGGVDHKKQFWRYFAGNLSG 120

QY 121 GAAGATSLCFVYPLDFARTLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
Db 121 GAAGATSLCFVYPLDFARTLAADVGKAGAREFEKGLGDCIVKIKYKSDGKGLYQGFNVS 180

QY 180 VQGIILYRAAYFGYDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYFPDFTVRERM 239
Db 181 VQGIILYRAAYFGYDTAKGMLPDPKKNTHIFISWMTAQSVTAVAGLLSYFPDFTVRERM 240

QY 240 QSGRKGADIMYTGTCWCKRIADGAKAPFKGANSVLRLGMCAGFVLVLYDEIKY 296
Db 241 QSGRKGADIMYTGTCWCKRIADGAKAPFKGANSVLRLGMCAGFVLVLYDEIKY 297

RESULT 7
ID ADT2 HUMAN STANDARD; PRT; 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence."
RL J. Biol. Chem. 265:16060-16063 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358 (1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,
RA Mazzarella R.A., Schlusser D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
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RA Becker M., Graves T., Ozersky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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CC
CC EMBL; M57424; AAA51737.1; -
CC EMBL; J02683; AAA35579.1; -
CC EMBL; L78810; AAB39286.1; -
CC EMBL; AC004000; AAB96347.1; -
CC EMBL; J03591; AAA36749.1; -
CC PIR; A29132; A29132.
CC Genew; HGNC:10991; SLC25A5.
CC MIM; 300150; -
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0015207; F:adenine transporter activity; TAS.
CC GO; GO:0006832; P:small molecule transport; TAS.
CC InterPro; IPR002067; Mit_carrier.
CC InterPro; IPR002030; Mit_uncoupling.
CC InterPro; IPR001993; Mitoch_carrier.
CC Pfam; PF00153; mito_carr; 3.
CC PRINTS; PR00926; MITOCARRIER.
CC PRINTS; PR00784; MTUNCOUPLING.
CC PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 6 6 V -> L (IN REF. 2).
FT CONFLICT 66 66 G -> E (IN REF. 2).
FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
FT CONFLICT 162 162 V -> G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 90.1%; Score 1398.5; DB 1; Length 298;
Best Local Similarity 88.9%; Pred. No. 5.8e-118;
Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

QY 1 MGDHAWSLKDFLAGAATAVSTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
Db 1 MTDAAVSPAKDFLAGGVAATAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60

QY 61 IPKEQGLSPWRGNLANVIRYFTQALNPAFKDKYKQLFLGGVDHKKQFWRYFAGNLSG 120
Db 61 IPKEQGLSPWRGNLANVIRYFTQALNPAFKDKYKQLFLGGVDHKKQFWRYFAGNLSG 120
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QY 121 GAAGATSLCPVYPLDPARTLAADVGR-AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179  
 DB 121 GAAGATSLCFVYPLDPARTLAADVGKAGAREFRGLDCLVKIKSDGKGLYQGFNVS 180  
 QY 180 VQGIILYRAAYFGVDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYPPDVRMM 239  
 DB 181 VQGIILYRAAYFGVDTAKGMLPDPKKNTHIVISWMTAQSVTAVAGLLSYPPDVRMM 240  
 QY 240 QSGRKADIMYTGTVDCWRKIADEGAKAFKFGANSVLRGMGAFVLYLDEIKKY 296  
 DB 241 QSGRKADIMYTGTVDCWRKIADEGKAFKFGANSVLRGMGAFVLYLDEIKKY 297

RESULT 8  
 ADT3 HUMAN  
 ID ADT3 HUMAN STANDARD; PRT; 298 AA.  
 AC P1236; Q96C49;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)  
 DE (Adenine nucleotide translocator 3) (ANT 3).  
 GN SLC25A6 OR ANT3  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89236396; PubMed=2541251;  
 RA Copens A.L., Runswick M.J., Walker J.E.;  
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial  
 RT ADP/ATP translocase.";  
 RL J. Mol. Biol. 206:261-280 (1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Zhou J., Yu W., Tang H., Mei G., Teang Y.T.M., Bouck J., Gibbs R.A.,  
 RA Margolin J.F.;  
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, Cervix, Eye, and Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Lakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinska M.I., Skalska U., Smalhus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RP SEQUENCE OF 36-298 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88124845; PubMed=2829183;  
 RA Houldsworth J., Attardi G.;  
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 RT level in adult human liver.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).  
 CC -|- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.

CC -|- SUBUNIT: Homodimer.  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -|- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -|- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC  
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 CC  
 CC EMBL: J03592; AAA36750.1; -;  
 CC EMBL: AY007135; AAG01998.1; -;  
 CC EMBL: BC007295; AAH07295.1; -;  
 CC EMBL: BC007850; AAH07850.1; -;  
 CC EMBL: BC008737; AAH08737.1; -;  
 CC EMBL: BC008935; AAH08935.1; -;  
 CC EMBL: BC014775; AAH14775.1; -;  
 CC FIR: S03894; S03894.  
 CC Genew: HGNC:10992; SLC25A6.  
 CC MIM: 300151; -;  
 CC MIM: 403000; -;  
 CC GO: GO:0005741; C:mitochondrial inner membrane translocase co. .; TAS.  
 CC GO: GO:0005471; P:ATP/ADP antiporter activity; NAS.  
 CC GO: GO:006854; P:ATP/ADP exchange; TAS.  
 CC InterPro: IPR002067; Mit\_carrier.  
 CC InterPro: IPR002030; Mit\_uncoupling.  
 CC InterPro: IPR001993; Mitoch\_carrier.  
 CC Pfam: PF00153; mito\_cartr; 3.  
 CC PRINTS: PR00926; MITOCARRIER.  
 CC PRINTS: PR00784; MTUNCOUPLING.  
 CC PROSITE: PS00215; MITOCH\_CARRIER; 3.  
 CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 100 1.  
 FT REPEAT 101 208 2.  
 FT REPEAT 209 298 3.  
 FT CONFLICT 105 108 KHTQ -> RHA (IN REF. 4).  
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).  
 SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0B49672F CRC64;  
 Query Match 89.2%; Score 1385.5; DB 1; Length 298;  
 Best Local Similarity 87.2%; Pred. No. 8.4e-117;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 MGDHAWSLFKDLGAVAAVSKTAVAPIERVKLLQVHASKQISAERQYKGIIDCVVR 60  
 DB 1 MTEQAISPAKDFLAGGIAAISKTAVERVKKLLQVHASKQIAADQYKGIIDCVR 60  
 QY 61 IPKEQGFSLFWRGNLAVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYFAGNLAG 120  
 DB 61 IPKEQGVLSFWRGNLAVIRYPTQALNPAFKDKYKQIFLGGVDKHTQFWRYFAGNLAG 120  
 QY 121 GAAGATSLCFVYPLDPARTLAADVGR-AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179  
 DB 121 GAAGATSLCFVYPLDPARTLAADVGKAGAREFRGLDCLVKIKSDGKGLYQGFNVS 180  
 QY 180 VQGIILYRAAYFGVDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYPPDVRMM 239  
 DB 181 VQGIILYRAAYFGVDTAKGMLPDPKKNTHIVISWMTAQSVTAVAGLLSYPPDVRMM 240  
 QY 240 QSGRKADIMYTGTVDCWRKIADEGAKAFKFGANSVLRGMGAFVLYLDEIKKY 297  
 DB 241 QSGRKADIMYTGTVDCWRKIADEGKAFKFGANSVLRGMGAFVLYLDEIKKY 298

```

RESULT 9
ADT3_BOVIN STANDARD; PRT; 298 AA.
ID ADT3_BOVIN STANDARD; PRT; 298 AA.
AC P32007;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
DE nucleotide translocator 3) (ANT 3).
GS SLC25A6 OR ANT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC -----
DR EMBL; M24103; AAA30769.1; -.
DR PIR; B43646; B43646.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carri; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 1C34E7DF6EDE4061 CRC64;

Query Match 88.9%; Score 1380.5; DB 1; Length 298;
Best Local Similarity 86.9%; Pred. No. 2.4e-116;
Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAATAAASVTAPIERVVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MTEQALSFADFLAGGIAAASVTAPIERVVKLLQVHASKQIAADKQYKGIIDCVI 60
QY 61 IPKEQGLSPWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGN 120
DB 61 IPKEQGLSPWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGN 120

```

## RESULT 10

## ADT\_DROME

## ID ADT\_DROME

## STANDARD; PRT; 299 AA.

## AC Q26365; P91614; Q26254; Q95S30; Q9VZ70;

## DT 15-JUL-1998 (Rel. 36, Created)

## DT 28-FEB-2003 (Rel. 41, Last sequence update)

## DT 15-SEP-2003 (Rel. 42, Last annotation update)

## DE ADP/ATP carrier protein (ADP/ATP translocase)

## DE translocator) (ANT) (Stress sensitive B protein).

## GN SESB OR A/T OR CG16944.

## OS Drosophila melanogaster (Fruit fly).

## OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

## OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

## OC Ephydroidea; Drosophilidae; Drosophila.

## OX NCBI\_TaxID=7227;

## RN [1]

## RP SEQUENCE FROM N.A.

## RX MEDLINE=92389367; PubMed=1387687;

## RA Louvi A., Tsililou S.G.;

## RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila

## RT melanogaster shows a high degree of similarity with the mammalian

## RT ADP/ATP translocases.";

## RL J. Mol. Evol. 35:44-50(1992).

## RN [2]

## RP SEQUENCE FROM N.A.

## RX MEDLINE=94350065; PubMed=7520869;

## RA Hutter P., Karch F.;

## RT "Molecular analysis of a candidate gene for the reproductive

## RT isolation between sibling species of Drosophila.";

## RL Experientia 50:749-762(1994).

## RN [3]

## RP SEQUENCE FROM N.A.

## RC STRAIN=Oregon-R;

## RA Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;

## RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

## RN [4]

## RP SEQUENCE FROM N.A.

## RC STRAIN=Berkley;

## RX MEDLINE=20196006; PubMed=10731132;

## RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,

## RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

## RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

## RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

## RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,

## RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,

## RA Ball J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

## RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

## RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

## RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

## RA Curtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

## RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

## RA de Carlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

## RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

## RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

## RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

## RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

## RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

## RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

## RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,





FT TRANSMEM 178 197 4 (POTENTIAL).  
FT TRANSMEM 216 233 5 (POTENTIAL).  
FT TRANSMEM 275 293 6 (POTENTIAL).  
SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;  
  
Query Match 74.9%; Score 1162.5; DB 1; Length 301;  
Best Local Similarity 76.9%; Pred. No. 7.9e-97;  
Matches 223; Conservative 26; Mismatches 40; Indels 1; Gaps 1;  
  
QY 6 WSLKDFLAGAVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVVRIPKEQ 65  
DB 8 YGFAKDFLAGISAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVVRIPKEQ 67  
  
QY 66 GFLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRFYFAGNLASGAAGA 125  
DB 68 GIGAFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRFYFAGNLASGAAGA 127  
  
QY 126 TSLCFVYPLDFARTLAAVGRRA-QREFHGLGDCIIFKPSDGLRGLYQGFNVSVQGI 184  
DB 128 TSLCFVYPLDFARTLAAVGRRA-QREFHGLGDCIIFKPSDGLRGLYQGFNVSVQGI 187  
  
QY 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDTPVRRMMQSGR 244  
DB 188 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDTPVRRMMQSGR 247  
  
QY 245 GADIMYTGTVDCWRKIAKDEGAKAFKPGAMSNVLRGMGGAFVLVLYDEIK 294  
DB 248 KSEVMYKNTLDCWKIKQEGSGGAFKPGAMSNVLRGMGGAFVLVLYDEIK 297  
  
RESULT 12  
ADT CHLKE  
ID ADT CHLKE STANDARD; PRT; 339 AA.  
AC P31592;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE ADP,ATP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT).  
OS Chlorella kessleri.  
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;  
OC Chlorellaceae; Chlorella.  
OX NCBI\_TaxID=3074;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92084708; PubMed=1748677;  
RA Hilgarth C., Sauer N., Tanner W.;  
RT "Glucose increases the expression of the ATP/ADP translocator and the glyceroldehyde-3-phosphate dehydrogenase genes in Chlorella.";  
RL J. Biol. Chem. 266:24044-24047(1991).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer (by similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
CC  
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CC  
CC EMBL; M76669; AAA33027.1; -.  
DR PIR; A41677; A41677.  
DR InterPro; IPR002067; Mit carrier.  
DR InterPro; IPR001993; Mitoch carrier.  
DR Pfam; PF00153; mito carr; 3.  
DR PRINTS; PS00926; MITOCARRIER.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
FT TRANSMEM 45 62 1 (POTENTIAL).  
FT TRANSMEM 108 126 2 (POTENTIAL).  
FT TRANSMEM 151 168 3 (POTENTIAL).  
FT TRANSMEM 209 228 4 (POTENTIAL).  
FT TRANSMEM 248 265 5 (POTENTIAL).  
FT TRANSMEM 304 322 6 (POTENTIAL).  
SQ SEQUENCE 339 AA; 36686 MW; 54779734A33B942 CRC64;  
  
Query Match 62.7%; Score 973.5; DB 1; Length 339;  
Best Local Similarity 65.3%; Pred. No. 7.6e-80;  
Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;  
  
QY 7 SFLKDFLAGAVAAVSKTAVAPIERVKLLQVQHASKOISAEK-QYKGIIDCVVRIPKE 64  
DB 40 AFVKLLAGTAGAISKTAIAPIERVKLLQVQHASKOISAEK-QYKGIIDCVVRIPKE 99  
  
QY 65 QGFLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRFYFAGNLASGAAGA 124  
DB 100 QGVASFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRFYFAGNLASGAAGA 158  
  
QY 125 ATSLCFVYPLDFARTLAAVGRRA-QREFHGLGDCIIFKPSDGLRGLYQGFNVSVQGI 184  
DB 159 AGSLLIVYPLDFARTLAAVGRRA-QREFHGLGDCIIFKPSDGLRGLYQGFNVSVQGI 218  
  
QY 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDTPVRRMMQSGR 243  
DB 219 VTRGAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDTPVRRMMQSGR 276  
  
QY 244 KGADIMYTGTVDCWRKIAKDEGAKAFKPGAMSNVLRGMGGAFVLVLYDEIKYV 297  
DB 277 -GGERQYNGTIDCWKRKIAKDEGAKAFKPGAMSNVLRGMGGAFVLVLYDEIKYV 329  
  
RESULT 13  
ADT CHLRE  
ID ADT CHLRE STANDARD; PRT; 308 AA.  
AC P27080;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE ADP,ATP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT).  
GN ABT.  
OS Chlamydomonas reinhardtii.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Chlamydomonadaceae; Chlamydomonas.  
OX NCBI\_TaxID=3055;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=FUD44-R2;  
RX MEDLINE=93204887; PubMed=8455552;  
RA Sharpe J.A., Day A.;  
RT "Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii.";  
RL Mol. Gen. Genet. 237:134-144(1993).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
CC  
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CC  
CC EMBL; X65194; CAA46311.1; -.





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CC EMBL; Z49974; CAA90275.1; -  
CC EMBL; AL023634; CAA19176.1; -  
CC PIR; T40526; T40526.  
DR GeneDB SPombe; SPBC530.10c; -  
DR InterPro; IPR002067; Mit\_carrier.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR Pfam; PF00153; mito\_carr; 3.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 2.  
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
FT TRANSMEM 28 48  
FT TRANSMEM 93 111  
FT TRANSMEM 131 151  
FT TRANSMEM 197 217  
FT TRANSMEM 222 242  
FT TRANSMEM 289 309  
SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;  
Query Match 48.5%; Score 752.5; DB 1; Length 322;  
Best Local Similarity 52.9%; Pred. No. 4.4e-60;  
Matches 156; Conservative 51; Mismatches 75; Indels 13; Gaps 6;  
QY 7 SLKDFLAGAANAAYSKTAVAPIERVKLLLOVQHASKQISAEEK---QYKGIIDCVVRIPK 63  
Db 26 TFFDFPMGVSAAVSKTAAAPIERVKLLIQN---DEMIRAGRLSHRYKIGIECFKRTAA 83  
QY 64 EQGFLSFWRGNLNIRVYPTQALNFAFKDKYKQLFLGGVDRHFKQFWRFYAGNLASGGAA 123  
Db 84 EGVISLWNGTANVIRYPTQALNFAFKDKYKQLFLGGVDRHFKQF---GYKKERDGYAKWFAAGLGGAA 142  
QY 124 GATSLCFVYPLDFARTLAAD---VGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
Db 143 GAASLLFVYSLDYARTLANDAKSAKKGGERQFNGLVYVRYKTYRSDGLRGLYRGFGPSV 202  
QY 181 QGIIIVRAAYFGVYDTAGK-MLPDPKNVHIFVSNWIAQSVTAVAGLLSYPPDTRRRMM 239  
Db 203 VGIVVYRGLYFGMDYTLKPVVILVGLGFLNGLAVTTGSGVAVSYPLDTRRRMM 262  
QY 240 QSGRKGADIMYGTVDCKWRKIAKDEGAKAFFKGAWSNVLKRGMGAPVLYVLYDEIK 294  
Db 263 TSGEA---VKYSSPECGRIILAKEGARSFFKAGANILRGVAGAGVLSIYDQVQ 314  
Search completed: December 30, 2003, 09:55:04  
Job time : 18 secs

QY 294 --KKY 296  
Db 378 FGKXY 382  
RESULT 15  
ADT\_SCHPO STANDARD; PRT; 322 AA.  
AC Q09188;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE ADP ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).  
GN ANCI OR SPBC530.10C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=96257204; PubMed=8675018;  
RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;  
RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae.";  
RL Gene 171:113-117(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Brooks J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown K., Brown D., Brown S., Chillingworth T., Church C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsis K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., McNeely P., Moulé S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Sesger K., Sharp S., Skellon J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Voicakert G., Aert R., Robben J., Grymonprez B., Waltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shipakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
RL "The genome sequence of Schizosaccharomyces pombe.";  
RL Nature 415:871-880(2002).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:51:26 ; Search time 41 Seconds  
(without alignments)  
1869.308 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHWSFLKDFLAGAVAAA.....LRGMGAFVLVLYBIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1464.5	94.3	298	6 O46373	O46373 oryctolagus
2	1462.5	94.2	298	11 Q8BV19	Q8BV19 mus musculus
3	1411.5	90.9	298	6 Q8SQH5	Q8SQH5 bos taurus
4	1392.5	89.7	298	13 Q8AYM3	Q8AYM3 gallus gall
5	1377.5	88.7	298	13 Q9VIC4	Q9VIC4 rana rugosa
6	1377.5	88.7	298	13 Q9PRH1	Q9PRH1 rana rugosa
7	1375.5	88.6	298	13 Q8JH10	Q8JH10 brachydontio
8	1374.5	88.5	298	13 Q9PRH2	Q9PRH2 rana rugosa
9	1366.5	88.0	298	13 Q9PRM9	Q9PRM9 xenopus lae
10	1245.5	80.2	299	5 Q95YX4	Q95YX4 ethmostigm
11	1241.5	79.9	300	5 Q9NHW5	Q9NHW5 lucilia cup
12	1241.5	79.9	312	5 Q8IRA0	Q8IRA0 drosophila
13	1234.5	79.5	317	13 Q91336	Q91336 rana sylvat
14	1183	76.2	288	5 O44094	O44094 drosophila
15	1183	76.2	288	5 O44093	O44093 drosophila
16	1180.5	76.0	254	11 Q8BKQ5	Q8BKQ5 mus musculus

17	1147	73.9	307	5	O62526	O62526 drosophila
18	1139.5	73.4	304	5	Q25129	Q25129 halocynthia
19	1101.5	70.9	315	4	Q9H0C2	Q9H0C2 homo sapien
20	1045.5	67.3	313	5	P91410	P91410 caenorhabdi
21	1043.5	67.2	313	5	Q21103	Q21103 caenorhabdi
22	1042	67.1	310	10	Q8H727	Q8H727 phytophthor
23	1037.5	66.8	300	5	O45865	O45865 caenorhabdi
24	1005.5	64.7	300	5	O01813	O01813 caenorhabdi
25	993.5	64.0	300	5	Q17407	Q17407 caenorhabdi
26	989.5	63.7	309	5	O97470	O97470 dictyosteli
27	959	61.8	307	8	Q9XM22	Q9XM22 ascaris suu
28	950	61.2	318	5	Q9BJ36	Q9BJ36 toxoplasma
29	926.5	59.7	301	5	Q8MVRA	Q8MVRA euploies sp
30	916.5	59.0	308	5	Q8MVR8	Q8MVR8 nyctotherus
31	914.5	58.9	305	5	Q8MVR7	Q8MVR7 nyctotherus
32	913.5	58.8	306	5	Q8MVR5	Q8MVR5 nyctotherus
33	908.5	58.5	301	5	Q81J34	Q81J34 plasmodium
34	906.5	58.4	308	5	Q8MVR6	Q8MVR6 nyctotherus
35	905.5	58.3	301	5	Q25692	Q25692 plasmodium
36	904.5	58.2	301	5	Q26006	Q26006 plasmodium
37	841.5	54.2	170	6	Q9XS69	Q9XS69 sus scrofa
38	772	49.7	306	5	Q18683	Q18683 caenorhabdi
39	757.5	48.8	305	3	Q9P8M1	Q9P8M1 varrowia li
40	750.5	48.3	307	5	Q76286	Q76286 trypanosoma
41	748.5	48.2	303	3	O74260	O74260 candida par
42	746.5	48.1	379	10	O49447	O49447 arabidopsis
43	745.5	48.0	326	5	P91270	P91270 caenorhabdi
44	743.5	47.9	307	5	Q26697	Q26697 trypanosoma
45	743	47.8	302	3	Q8J0M2	Q8J0M2 varrowia li

#### ALIGNMENTS

RESULT 1

O46373	ID	O46373	PRELIMINARY;	PRT;	298 AA.
AC	O46373;				
DT	01-JUN-1998 (TREMBLrel. 06, Created)				
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	ADP/ATP translocase.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TaxID=9986;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skeletal muscle;				
RA	Yamaguchi N., Kasai M.;				
RT	"Identification of a 30kDa calsequestrin-binding protein, which				
RT	regulates calcium release from sarcoplasmic reticulum of rabbit				
RT	skeletal muscle.";				
RL	J. Biochem. 335:541-547 (1998).				
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.				
DR	EMBL; AB009386; BAA23777.1; -				
DR	InterPro: IPR001993; Mitoch carrier.				
DR	InterPro: IPR002067; Mit carrier.				
DR	PIfam; PF00153; mito_carr; 3.				
DR	PRINTS; PR00926; MITOCARRIER.				
DR	PRINTS; PR00784; MTUNCOUPLING.				
DR	PROSITE; PS00215; MITOCH CARRIER; 3.				
KW	Membrane; Transmembrane; Transport				
SQ	SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;				

Query Match 94.3%; Score 1464.5; DB 6; Length 298;  
Best Local Similarity 94.6%; Pred. No. 7.2e-129;  
Matches 282; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAVAAVSKTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60

DB 1 MSDQALSFLKDFLAGGVAAVSKTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60

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QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLASG 120
DE |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OS |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_SEQUENCE FROM N.A.
RP YAMAZAKI N., SHINOHARA Y., TANIDA K., TERADA H.;
RA "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT identification of possible amino acids that determine functional
RT differences in its isoforms.";
RL Mitochondrion 1:371-379(2002).
DR EMBL; AB065433; BAB84673.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match 90.9%; Score 1411.5; DB 6; Length 298;
Best Local Similarity 89.9%; Pred. No. 6.6e-124;
Matches 267; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAATAVSKTAVPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLASG 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GAAGATSLCFVYPLDFARTLAADVRR-AQREFHGLGDCIIKPKSDGLRGLYQGFNVS 179
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GAAGATSLCFVYPLDFARTLAADVRR-AQREFHGLGDCIIKPKSDGLRGLYQGFNVS 180
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 VOGIIYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMM 239
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 VOGIIYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMM 240
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 QSGRKADIMYTGTCWCKRIADKAGAFKPGAWSNVLKRGMGGAFLVLYDEIKKY 296
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 QSGRKADIMYTGTCWCKRIADKAGAFKPGAWSNVLKRGMGGAFLVLYDEIKKY 297
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
Q8AYM3 PRELIMINARY; PRT; 298 AA.
ID Q8AYM3;
AC Q8AYM3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE ATP/ADP antiporter.
GN AVANT.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_SEQUENCE FROM N.A.
RP TOYOMIZU M., UEDA M., SATO S., SEKI Y., SATO K., AKIBA Y.;
RA "Cold-induced mitochondrial uncoupling and expression of chicken UCP
RT and ANT mRNA in chicken skeletal muscle.";
RL FEBS Lett. 0:0-0(2002).
DR EMBL; AB088686; BAC15533.1; -.
SQ SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;

Query Match 89.7%; Score 1392.5; DB 13; Length 298;
Best Local Similarity 88.3%; Pred. No. 4e-122;
Matches 263; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAATAVSKTAVPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60

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QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLASG 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLASG 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GAAGATSLCFVYPLDFARTLAADVRR-AQREFHGLGDCIIKPKSDGLRGLYQGFNVS 179
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GAAGATSLCFVYPLDFARTLAADVRR-AQREFHGLGDCIIKPKSDGLRGLYQGFNVS 180
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 VOGIIYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMM 239
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 VOGIIYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMM 240
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 QSGRKADIMYTGTCWCKRIADKAGAFKPGAWSNVLKRGMGGAFLVLYDEIKKY 297
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 QSGRKADIMYTGTCWCKRIADKAGAFKPGAWSNVLKRGMGGAFLVLYDEIKKY 298
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
Q8SQH5 PRELIMINARY; PRT; 298 AA.
ID Q8SQH5;
AC Q8SQH5;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

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Db 1 MADQALSLKDFLARGVAAAIKSTAVAPIERVLKLLQVQHASQIAADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQFLGGVDHKKQFWRYPAGNLASG 120
Db 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQFLGGVDHKKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTLAADVGR--AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
Db 121 GAAGATSLCFVYPLDPARTLAADVGR--AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 239
Db 181 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
Db 241 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 5
Q9YIC4 PRELIMINARY; PRT; 298 AA.
ID Q9YIC4
AC Q9YIC4
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Winkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008457; BAA36507.1; -.
DR EMBL; AB008456; BAA36506.1; -.
DR EMBL; AB008461; BAA36511.1; -.
DR EMBL; AB008462; BAA36512.1; -.
DR InterPro; IPR001993; Mitoch. carrier.
DR InterPro; IPR002067; Mit. carrier.
DR InterPro; IPR002030; Mit uncoupling.
DR Pfam; PF00153; mito carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 88.7%; Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%; Pred. No. 1e-120;
Matches 259; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGVAAAVKSTAVAPIERVLKLLQVQHASQIAADKQYKGIIDCVVR 60
Db 1 MTDALISFAKDFLAGGVAIAIKSTAVAPIERVLKLLQVQHASQIATADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQFLGGVDHKKQFWRYPAGNLASG 120
Db 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQFLGGVDHKKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTLAADVGR--AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
Db 121 GAAGATSLCFVYPLDPARTLAADVGR--AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 239
Db 181 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
Db 241 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 7
Q8JH10 PRELIMINARY; PRT; 298 AA.
ID Q8JH10
AC Q8JH10
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Solute carrier family 25 member 5 protein.
GN SLC25A5.
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Db 241 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 6
Q9PRH1 PRELIMINARY; PRT; 298 AA.
ID Q9PRH1
AC Q9PRH1
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Winkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BAA36513.1; -.
DR EMBL; AB008456; BAA36506.1; -.
DR EMBL; AB008461; BAA36511.1; -.
DR EMBL; AB008462; BAA36512.1; -.
DR InterPro; IPR001993; Mitoch. carrier.
DR InterPro; IPR002067; Mit. carrier.
DR InterPro; IPR002030; Mit uncoupling.
DR Pfam; PF00153; mito carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 88.7%; Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%; Pred. No. 1e-120;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGVAAAVKSTAVAPIERVLKLLQVQHASQIAADKQYKGIIDCVVR 60
Db 1 MTDALISFAKDFLAGGVAIAIKSTAVAPIERVLKLLQVQHASQIATADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQFLGGVDHKKQFWRYPAGNLASG 120
Db 61 IPKEQGLSFWRGNLNANVIRYPTQALNFAKDKYKQFLGGVDHKKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTLAADVGR--AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
Db 121 GAAGATSLCFVYPLDPARTLAADVGR--AOREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 239
Db 181 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDVTVRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
Db 241 QSGRKGADIMYTGTVDCWRKIADKAGAPFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 7
Q8JH10 PRELIMINARY; PRT; 298 AA.
ID Q8JH10
AC Q8JH10
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Solute carrier family 25 member 5 protein.
GN SLC25A5.
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Db 1 MTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKHKGIMDCVVR 60
QY 61 IPKEQGFSLFWRGNLNANVIRYPTQALNFAFKDKYKQLFLGGVDHKKQFWRYFAGNLASG 120
Db 61 IPKEQGFVSEWRGNLANVIRYPTQALNFAFKDKYKIFLDNDVDDKQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADVGRRA-ORFPHGLGDCIIKIFKSDGLRGLYQGFNVNS 179
Db 121 GAAGATSLCFVYPLDFARTLADVGRGANEREFKGLGDCIVKISKSDGIGKGLYQGFNVNS 180
QY 180 VQGIIIRAAVFGYVDTAKGMLDPPKKNVHIFVSWMTAQSVTAVAGLLSYPPDVRMRMM 239
Db 181 VQGIIIRAAVFGYVDTAKGMLDPPKKNTHIFVSWMTAQSVTAVAGFASYPDVRMRMM 240
QY 240 QSGRKGADIMYTGTCWRKRIADDEGAKAFKPGKAWSNVLRGMGGAFFVLVLYDEIKKYV 297
Db 241 QSGRKGADIMYTGTCWKRIARDESKAFKPGKAWSNVLRGMGGAFFVLVLYDEIKKYV 298

RESULT 10
Q95VX4 PRELIMINARY; PRT; 299 AA.
AC Q95VX4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP-ATP translocator.
OS Ethmostigmus rubripes.
OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
OX NCBI_TaxID=62613;
RN 1;
RP SEQUENCE FROM N.A.
RA Burnell J.N.;
RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus rubripes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401758; AAL02100.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carri; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
DR MEMBRANE; Transmembrane; Transport.
SQ SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E CRC64;

Query Match 80.28; Score 1245.5; DB 5; Length 299;
Best Local Similarity 80.3%; Pred. No. 2.3e-108;
Matches 236; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

QY 5 AWSFLKDFLAGVAAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVRIKPE 64
Db 5 AWSFLKDFIAGVAAAIKSTAVAPIERVKLLQVQHASKQIADVQYKGMVDFCVRIKPE 64
QY 65 QGFLSWRGNLNANVIRYPTQALNFAFKDKYKQLFLGGVDHKKQFWRYFAGNLASGAAG 124
Db 65 QGILSYWRGNLANVIRYPTQALNFAFKDKYKIFLGGVDKRTQFWRYFLGNLASGAAG 124
QY 125 ATSLCFVYPLDFARTLADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVNSVQGI 183
Db 125 ATSLCFVYPLDFARTLADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVNSVQGI 184
QY 184 IIVRAAYFGYVDTAKGMLDPPKKNVHIFVSWMTAQSVTAVAGLLSYPPDVRMRMMQSGR 243
Db 185 IIVRAAYFGYVDTAKGMLDPPKKNTPVIVISWIIAQVTTTCAGIISYPDVRMRMMQSGR 244
QY 244 KGADIMYTGTCWRKRIADDEGAKAFKPGKAWSNVLRGMGGAFFVLVLYDEIKKYV 297
Db 245 KKADILYKNTIDCWGKIYKTEGGAAPFKGAFSNILRGTGGAFFVLVLYDEIKALI 298

RESULT 11
Q9NHWS PRELIMINARY; PRT; 300 AA.
ID Q9NHWS

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AC Q9NHWS;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=SS mal seeking;
RA Chen Z., Fair J.A., Batterham P.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF218587; AAF3322.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carri; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
DR MEMBRANE; Transmembrane; Transport.
SQ SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;

Query Match 79.9%; Score 1241.5; DB 5; Length 300;
Best Local Similarity 78.7%; Pred. No. 5.6e-108;
Matches 236; Conservative 25; Mismatches 36; Indels 3; Gaps 1;

QY 1 MGDHAAA-WSFLKDFLAGVAAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDC 57
Db 1 MCKEADPLGFKVDFPAAGGISAASVKTAVAPIERVKLLQVQHASKQISPDQYKGMIDC 60
QY 58 VVRIPKEQGFSLFWRGNLNANVIRYPTQALNFAFKDKYKQLFLGGVDHKKQFWRYFAGNL 117
Db 61 FVRIPKEQGFASVWRGNMANVIRYPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFLGNL 120
QY 118 ASGGAAGATSLCFVYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFN 177
Db 121 ASGGAAGATSLCFVYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFN 180
QY 178 VSVQGIIRAAVFGYVDTAKGMLDPPKKNVHIFVSWMTAQSVTAVAGLLSYPPDVRMRM 237
Db 181 VSVQGIIRAAVFGYVDTARGMLDPPKKNTPVIVISWIIAQVTTVAGIISYPDVRMRM 240
QY 238 MQSGRKGADIMYTGTCWRKRIADDEGAKAFKPGKAWSNVLRGMGGAFFVLVLYDEIKKYV 297
Db 241 MMQSGRKATEIIVKNTLHCWATIAKQEGTGAFKGAFFSNVLRGTGGAFFVLVLYDEIKKPL 300

RESULT 12
Q8IRA0 PRELIMINARY; PRT; 312 AA.
ID Q8IRA0;
AC Q8IRA0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG16944-PC.
GN SESB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,

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Db 121 GAAGATSLCFVYPLDFARTLRLAADVGKAGAGREFNGLGDCIAKIFKSDGLKGLYQGFNVS 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDVTVRMM 239
Db 181 VQGIILYRAAYFGIYDTAKGMLPDPKNTHIFVSWMIAQSVTAVAGSGSPFDIVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADKDEKAFKK 271
Db 241 QSGRKGAEIMYSOTIDCWKKIARDEGGRAFFR 272

RESULT 14
O44094 PRELIMINARY; PRT; 288 AA.
AC O44094;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE ADP/ATP translocase (fragment).
GN SESB.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Coneron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR FlyBase; FBgn0023237; Dsub\esb.
DR InterPro; IPR001993; Mitoch.carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT NON TER 288
SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E47781B26 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
Best Local Similarity 79.6%; Pred. No. 1.6e-102;
Matches 226; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

QY 5 AWSFLKDFLAGAATAVAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRIKPE 64
Db 7 AMGFKDFAAGGISAASVKTAVAPIERVKLLQVQHASKOISAEKQYKGMVDCFIKPE 66
QY 65 QGFLSFWRGNLNVIYFFPTQALNFAFKDKYKQFLGGVDHKKQFWRYFAGNLASGGAAG 124
Db 67 QGFSSFWRGNLNVIYFFPTQALNFAFKDKYKQFLGGVDHKKQFWRYFAGNLASGGAAG 126
QY 125 ATSLCFVYPLDFARTLRLAADVGRRARQREPHGLGDCIIFKPSDGLRGLYQGFNVVQGI 184
Db 127 ATSLCFVYPLDFARTLRLAADVGRRARQREPHGLGDCIIFKPSDGLRGLYQGFNVVQGI 186
QY 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDVTVRMM 244
Db 187 IYRAAYFGFYDTAR-MLPDPKNTPYISWAIQAQVTTVAGISVYPPDVTVRMM 245
QY 245 GADIMYTGTVDCWRKIADKDEKAFKKGAWSNVLRGMGGAFVLV 288
Db 246 ATEIIYNTHCHGTAKQEGT-AFFKGAFSNVLRGTGGAFVLV 288

Search completed: December 30, 2003, 09:56:54
Job time : 43 secs

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Db 121 GAAGATSLCFVYPLDFARTLRLAADVGKAGAGREFNGLGDCIAKIFKSDGLKGLYQGFNVS 180
QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDVTVRMM 239
Db 181 VQGIILYRAAYFGIYDTAKGMLPDPKNTHIFVSWMIAQSVTAVAGSGSPFDIVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADKDEKAFKK 271
Db 241 QSGRKGAEIMYSOTIDCWKKIARDEGGRAFFR 272

RESULT 15
O44093 PRELIMINARY; PRT; 288 AA.
AC O44093;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE ADP/ATP translocase (fragment).
GN SESB.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Coneron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR FlyBase; FBgn0023237; Dsub\esb.
DR InterPro; IPR001993; Mitoch.carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT NON TER 288
SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E47781B26 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
Best Local Similarity 79.6%; Pred. No. 1.6e-102;
Matches 226; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

QY 5 AWSFLKDFLAGAATAVAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRIKPE 64
Db 7 AMGFKDFAAGGISAASVKTAVAPIERVKLLQVQHASKOISAEKQYKGMVDCFIKPE 66
QY 65 QGFLSFWRGNLNVIYFFPTQALNFAFKDKYKQFLGGVDHKKQFWRYFAGNLASGGAAG 124
Db 67 QGFSSFWRGNLNVIYFFPTQALNFAFKDKYKQFLGGVDHKKQFWRYFAGNLASGGAAG 126
QY 125 ATSLCFVYPLDFARTLRLAADVGRRARQREPHGLGDCIIFKPSDGLRGLYQGFNVVQGI 184
Db 127 ATSLCFVYPLDFARTLRLAADVGRRARQREPHGLGDCIIFKPSDGLRGLYQGFNVVQGI 186
QY 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDVTVRMM 244
Db 187 IYRAAYFGFYDTAR-MLPDPKNTPYISWAIQAQVTTVAGISVYPPDVTVRMM 245
QY 245 GADIMYTGTVDCWRKIADKDEKAFKKGAWSNVLRGMGGAFVLV 288
Db 246 ATEIIYNTHCHGTAKQEGT-AFFKGAFSNVLRGTGGAFVLV 288

Search completed: December 30, 2003, 09:56:54
Job time : 43 secs

```

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 09:54:41 ; Search time 21 Seconds  
(without alignments)  
598.396 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHWSFLKDFLAGAVAAA.....LRGMGAFVLVLYDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pdp.\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pdp.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pdp.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pdp.\*

5: /cgn2\_6/ptodata/1/iaa/PTCTUS COMB.pdp.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1553	100.0	297	4	US-09-434-354-47
2	1457.5	93.9	298	3	US-08-961-871-10
3	1391.5	89.6	298	4	US-09-434-354-48
4	1385.5	89.2	298	4	US-09-434-354-49
5	304	19.6	469	4	US-09-996-243-289
6	301	19.4	469	3	US-09-188-930-339
7	301	19.4	469	4	US-09-312-283C-339
8	291	18.7	447	4	US-09-160-119-4
9	291	18.7	674	4	US-09-160-119-2
10	267	17.2	291	4	US-09-501-558-2
11	265.5	17.1	335	4	US-09-482-273-118
12	238	15.3	320	2	US-08-933-750C-12
13	238	15.3	320	3	US-09-234-613-12
14	233.5	15.0	312	3	US-09-142-565-2
15	227	14.6	299	1	US-08-518-878B-56
16	227	14.6	299	2	US-08-470-868A-56
17	227	14.6	309	1	US-08-518-878B-51
18	227	14.6	309	2	US-08-807-861A-51
19	227	14.6	309	2	US-08-470-868A-51
20	227	14.6	309	3	US-09-210-681-51
21	227	14.6	309	3	US-08-946-719A-51
22	227	14.6	309	4	US-09-547-983-51
23	227	14.6	311	2	US-08-775-009-33
24	225	14.5	311	2	US-08-775-009-32
25	222.5	14.3	308	2	US-08-937-466-2
26	222.5	14.3	308	2	US-09-172-528-2
27	222.5	14.3	308	3	US-09-318-199-2
28	222.5	14.3	308	3	US-09-503-579-2
29	218.5	14.1	308	2	US-08-937-466-4
30	218.5	14.1	308	2	US-09-172-528-4
31	218.5	14.1	308	2	US-09-318-199-4
32	218.5	14.1	308	2	US-09-503-579-4
33	208.5	13.4	293	4	US-09-501-558-4
34	196.5	12.7	307	2	US-08-807-861A-56
35	196.5	12.7	307	3	US-09-210-681-56
36	196.5	12.7	307	3	US-08-946-719A-56
37	196.5	12.7	307	4	US-09-547-983-56
38	193	12.4	303	1	US-08-294-522B-36
39	192	12.4	303	1	US-08-518-878B-37
40	192	12.4	303	2	US-08-807-861A-37
41	192	12.4	303	2	US-08-470-868A-37
42	192	12.4	303	3	US-09-210-681-37
43	192	12.4	303	3	US-08-946-719A-37
44	192	12.4	303	4	US-09-547-983-37
45	190.5	12.3	306	5	PCT-US94-09799-1

RESULT 1

US-09-434-354-47

; Sequence 47, Application US/09434354

; Patent No. 6562563

; GENERAL INFORMATION:

; APPLICANT: Murphy, Anne N.

; APPLICANT: Cleverger, William

; APPLICANT: Wiley, Sandra Eileen

; APPLICANT: Andreyev, Alexander Y.

; APPLICANT: Frigeri, Luciano G.

; APPLICANT: Velicelbi, Gonul

; APPLICANT: Davis, Robert E.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING

; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR

; FILE REFERENCE: 660088.433

; CURRENT APPLICATION NUMBER: US/09/434,354

; CURRENT FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 47

; LENGTH: 297

; TYPE: PRT

; ORGANISM: Homo sapien

; US-09-434-354-47

Query Match 100.0%; Score 1553; DB 4; Length 297;

Best Local Similarity 100.0%; Pred.No. 4.2e-172;

Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGDHWSFLKDFLAGAVAAVSKTAVPIERVKLLQVHASKQISAEKQYKGIIDCVR 60

Db 1 MGDHWSFLKDFLAGAVAAVSKTAVPIERVKLLQVHASKQISAEKQYKGIIDCVR 60

Qy 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120

Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120

Qy 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIPKSDGLRGLYQGFNVSV 180

Db 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIPKSDGLRGLYQGFNVSV 180

Qy 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDTRRRMMQ 240

Db 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWIAQSVTAVAGLLSYPPDTRRRMMQ 240

Qy 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKPGAWSNVLRCMGAFVLVLYDEIKKYV 297

Db 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKPGAWSNVLRCMGAFVLVLYDEIKKYV 297

ALIGNMENTS

RESULT 2  
 US-08-961-871-10  
 ; Sequence 10, Application US/08961871  
 ; Patent No. 6013858  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wallace, Douglas C.  
 ; APPLICANT: Graham, Brett H.  
 ; APPLICANT: Macgregor, Grant R.  
 ; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine  
 ; Nucleotide Translocator Protein and Methods  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
 ; STREET: 5370 Manhattan Circle, Suite 201  
 ; CITY: Boulder  
 ; STATE: Colorado  
 ; COUNTRY: US  
 ; ZIP: 80303  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/961,871  
 ; FILING DATE: 31-OCT-1997  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/030,017  
 ; FILING DATE: 01-NOV-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ferber, Donna M.  
 ; REGISTRATION NUMBER: 33,878  
 ; REFERENCE/DOCKET NUMBER: 78-96  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 499-8080  
 ; TELEFAX: (303) 499-8089  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 298 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-961-871-10

Query Match 93.9%; Score 1457.5; DB 3; Length 298;  
 Best Local Similarity 93.6%; Pred. No. 5.4e-161;  
 Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;  
 QY 1 MGDHWSFLKDFLAGAATAVAPIERVVLLQVHASKQISAEKQYKGIIDCVVR 60  
 DB 1 MGDHWSFLKDFLAGAATAVAPIERVVLLQVHASKQISAEKQYKGIIDCVVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLSG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLSG 120  
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFFHGLGDCIIKI FKS DGLRGLYQGFNVS 179  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFFHGLGDCIIKI FKS DGLRGLYQGFNVS 180  
 QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSTVAVAGLSYFPDTRRRMM 239  
 DB 181 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSTVAVAGLSYFPDTRRRMM 240  
 QY 240 QSGRKGADIMYTGTVDCWRKIADEGAKAPFKGANSNVLKRGMGAFVLYLDEIKKY 297  
 DB 241 QSGRKGADIMYTGTVDCWRKIADEGAKAPFKGANSNVLKRGMGAFVLYLDEIKKY 298

RESULT 3  
 US-09-434-354-48

; Sequence 48, Application US/09434354  
 ; Patent No. 6562563  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murphy, Anne N.  
 ; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Andreyev, Alexander Y.  
 ; APPLICANT: Frigeri, Luciano G.  
 ; APPLICANT: Velicelebi, Gonul  
 ; APPLICANT: Davis, Robert E.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
 ; INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
 ; IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
 ; FILE REFERENCE: 660088.433  
 ; CURRENT APPLICATION NUMBER: US/09/434,354  
 ; CURRENT FILING DATE: 1999-11-03  
 ; NUMBER OF SEQ ID NOS: 54  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 48  
 ; LENGTH: 298  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-09-434-354-48

Query Match 89.6%; Score 1391.5; DB 4; Length 298;  
 Best Local Similarity 88.6%; Pred. No. 2.5e-153;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 MGDHWSFLKDFLAGAATAVAPIERVVLLQVHASKQISAEKQYKGIIDCVVR 60  
 DB 1 MGDHWSFLKDFLAGAATAVAPIERVVLLQVHASKQISAEKQYKGIIDCVVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLSG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDVDRHKQFWRYPAGNLSG 120  
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFFHGLGDCIIKI FKS DGLRGLYQGFNVS 179  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREFFHGLGDCIIKI FKS DGLRGLYQGFNVS 180  
 QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSTVAVAGLSYFPDTRRRMM 239  
 DB 181 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSTVAVAGLSYFPDTRRRMM 240  
 QY 240 QSGRKGADIMYTGTVDCWRKIADEGAKAPFKGANSNVLKRGMGAFVLYLDEIKKY 296  
 DB 241 QSGRKGADIMYTGTVDCWRKIADEGAKAPFKGANSNVLKRGMGAFVLYLDEIKKY 297

RESULT 4  
 US-09-434-354-49  
 ; Sequence 49, Application US/09434354  
 ; Patent No. 6562563  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murphy, Anne N.  
 ; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Andreyev, Alexander Y.  
 ; APPLICANT: Frigeri, Luciano G.  
 ; APPLICANT: Velicelebi, Gonul  
 ; APPLICANT: Davis, Robert E.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
 ; INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
 ; IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
 ; FILE REFERENCE: 660088.433  
 ; CURRENT APPLICATION NUMBER: US/09/434,354  
 ; CURRENT FILING DATE: 1999-11-03  
 ; NUMBER OF SEQ ID NOS: 54  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 49  
 ; LENGTH: 298  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien



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/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089599
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089600
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089653
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/089907
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/089908
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/089947
/ PRIOR FILING DATE: 1998-06-19
/ PRIOR APPLICATION NUMBER: 60/089948
/ PRIOR FILING DATE: 1998-06-19
/ PRIOR APPLICATION NUMBER: 60/089952
/ PRIOR FILING DATE: 1998-06-19
/ PRIOR APPLICATION NUMBER: 60/090246
/ PRIOR FILING DATE: 1998-06-22
/ PRIOR APPLICATION NUMBER: 60/090252
/ PRIOR FILING DATE: 1998-06-22
/ PRIOR APPLICATION NUMBER: 60/090254
/ PRIOR FILING DATE: 1998-06-22
/ PRIOR APPLICATION NUMBER: 60/090349
/ PRIOR FILING DATE: 1998-06-23
/ PRIOR APPLICATION NUMBER: 60/090355
/ PRIOR FILING DATE: 1998-06-23
/ PRIOR APPLICATION NUMBER: 60/090429
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090431
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090435
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090444
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090445
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090472
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090535
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090540
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090542
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090676
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090678
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090690
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090694
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090695
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090696
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090862
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: 60/090863
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: 60/091360
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091478
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091544
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091519
/ PRIOR FILING DATE: 1998-07-02

/ PRIOR APPLICATION NUMBER: 60/091626
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091633
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091978
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match      19.6%; Score 304; DB 4; Length 469;
Best Local Similarity 29.0%; Pred. No. 1.4e-26;
Matches 88; Conservative 58; Mismatches 115; Indels 42; Gaps 11;

QY      6 WSPKDFLAGAAVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVVRIPKEQ 65
Db      187 WRHL---VAGGGAGAVSRCTCTAPLDRKLVLMQV---HASR-----SNNNGIVGGFTQMIREG 237

QY      66 GFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDR-----HKQFWRYFAGNLASG 120
Db      238 GARSLSWRGNGINVLKIAPESAIKFMAYEQIKRLV--GSDQETLRIHER-----LVAG 287

QY      121 GAAGATSLCFVYPLDPAFTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
Db      288 SLAGATAQSSIVPMEVLKTRMAL-----RKTQGYSGMLDCARRILAREGVAAFYKGYVPMN 343

QY      181 QGIIIVRAAYFGVYDTAKGM-----LPDPKNVHFVSWMTAQSVTAVAGLSYFPDT 232
Db      344 LGIIPYAGIDLAVYETLKNALQHVAVNSADP---GVFVLLACGTTMSSTCGQLASYPLAL 400

QY      233 VRRMMQSGRKGDIMYTGTVDCWFKIAKDEGAKAPFKGANSVLRGMGAFV-LVLYD 291
Db      401 VTRMQAQSIEGAPVETWSSL--FKHILRTGAGFLYRGLAPNFMKVIPAVSISYVVE 458

QY      292 EIK 294
Db      459 NLK 461

RESULT 6
US-09-188-930-339
/ Sequence 339, Application US/09188930A
/ Patent No. 6150502
/ GENERAL INFORMATION:
/ APPLICANT: Watson, James D.
/ APPLICANT: Strachan, Lorna
/ APPLICANT: Sleeman, Matthew
/ APPLICANT: Onrust, Rene
/ APPLICANT: Murison, James Greg
/ TITLE OF INVENTION: Compositions Isolated From Skin Cells
/ TITLE OF INVENTION: and Methods For Their Use
/ FILE REFERENCE: 11000.1011c1
/ CURRENT APPLICATION NUMBER: US/09/188,930A
/ CURRENT FILING DATE: 1998-11-09
/ NUMBER OF SEQ ID NOS: 348
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 339
/ LENGTH: 469
/ TYPE: PRT
/ ORGANISM: Mouse
US-09-188-930-339

Query Match      19.4%; Score 301; DB 3; Length 469;
Best Local Similarity 28.9%; Pred. No. 3e-26;
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;

QY      6 WSPKDFLAGAAVAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVV-----RI 61
Db      187 WRHL---VAGGGAGAVSRCTCTAPLDRKLVLMQV---HASRNNM-----CIVGGFTQM 233

QY      62 PKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDR-----HKQFWRYFAGN 116
Db      116 PKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDR-----HKQFWRYFAGN 116
```

Db 234 IREGGAKSLWRGNGINVLKIAPESAIKFMAYEQMKRLV--GSDQETLRIHER----- 283  
QY 117 LASGGAAGATSLCFVYPLDPFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGF 176  
Db 284 LVAGSLAGAIAQSSIFPMEVLKTRMAL----RTGQYSGMLDCARRILAKEGVAAPYKGY 339  
QY 177 NVSVQGIIRAAAYFGYDITAKG-----LPDPKNVHIFVSWMIAQSVTAVAG-LLS 227  
Db 340 IPNMLGIIPVAGIDLAVYETLKNLTQRYAVNSADP---GVFV-LLACGTFISSTCCQLAS 395  
QY 228 YPFDTVRRMMMSQSGKADIMYTGIVDCHWKIAKDEGAKAFKPGAWNSVLRGMGAFV- 286  
Db 396 YPALVTRTRMQAASIEGAEVMTSSL--FKQILRTEGAFGLYRGLAPNPMKVIPAVSIS 453  
QY 287 LVLYDEIK 294  
Db 454 YVYENLK 461

## RESULT 7

US-09-312-283C-339  
; Sequence 339, Application US/09312283C  
; Patent No. 6573095

## GENERAL INFORMATION:

; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James G.  
; APPLICANT: Kumble, Krishanand D.  
; TITLE OF INVENTION: Compositions Isolated from Skin Cells  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1011c2  
; CURRENT APPLICATION NUMBER: US/09/312,283C  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 425  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 339  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Mouse

US-09-312-283C-339

Query Match 19.4%; Score 301; DB 4; Length 469;  
Best Local Similarity 28.9%; Pred. No. 3e-26;  
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;

QY 6 WSPFKDPLAGAVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVV----RI 61  
Db 187 WRHL---VAGGGAGAVSRTCTAPDLRLKVLNQV-HASRSNNM-----CIVGGFTQM 233  
QY 62 PKEGFLSFRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDR-----HKQFWRYPAGN 116  
Db 234 IREGGAKSLWRGNGINVLKIAPESAIKFMAYEQMKRLV--GSDQETLRIHER----- 283  
QY 117 LASGGAAGATSLCFVYPLDPFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGF 176  
Db 284 LVAGSLAGAIAQSSIFPMEVLKTRMAL----RTGQYSGMLDCARRILAKEGVAAPYKGY 339  
QY 177 NVSVQGIIRAAAYFGYDITAKG-----LPDPKNVHIFVSWMIAQSVTAVAG-LLS 227  
Db 340 IPNMLGIIPVAGIDLAVYETLKNLTQRYAVNSADP---GVFV-LLACGTFISSTCCQLAS 395  
QY 228 YPFDTVRRMMMSQSGKADIMYTGIVDCHWKIAKDEGAKAFKPGAWNSVLRGMGAFV- 286  
Db 396 YPALVTRTRMQAASIEGAEVMTSSL--FKQILRTEGAFGLYRGLAPNPMKVIPAVSIS 453  
QY 287 LVLYDEIK 294  
Db 454 YVYENLK 461

## RESULT 8

Query Match 18.7%; Score 291; DB 4; Length 674;

US-09-160-119-4  
; Sequence 4, Application US/09160119A  
; Patent No. 6316219  
; GENERAL INFORMATION:  
; APPLICANT: KRIEF, STEPHANE  
; APPLICANT: SOUCHET, MICHEL  
; APPLICANT: BRIL, ANTOINE  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30985  
; CURRENT APPLICATION NUMBER: US/09/160,119A  
; CURRENT FILING DATE: 1998-09-24  
; EARLIER APPLICATION NUMBER: EP 97402511.6  
; EARLIER FILING DATE: 1997-10-23  
; EARLIER APPLICATION NUMBER: EP 98401655.0  
; EARLIER FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS

Query Match 18.7%; Score 291; DB 4; Length 447;  
Best Local Similarity 27.5%; Pred. No. 4.1e-25;  
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;  
QY 12 FLAGVAAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIKPEQGFLSPW 71  
Db 104 FGLGSVAGAVGATVYPIDLVTRMQNRSTGSGFVGLMYKNSFDCPKKVLRYEGPFLY 163  
QY 72 RGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLSGGAAGATSLCFV 131  
Db 164 RGLLPOLLGVAPEKAIKLTVDNDFVRDKFM-----HKDGSVPLAAEILAGCAGGSQVIFT 218  
QY 132 YPLDPARTL--AADV--GRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIR 187  
Db 219 NPLEIVKIRLQVAGEITTGPRVS-----ALSVVRDLGFFGIYKAKACFLRDIPPS 269  
QY 188 AAYFGYVDYAKGMLPDPKNVHIFVSWMIAQSVTAV-AGLLSYFPTDVRMMMSQSGRKA 246  
Db 270 AIYFPCYAHVQASFANEDQVSGSLLLAGATAGMPAASLVTPADVIKTR--LQVAARAG 327  
QY 247 DIMYTGTVDCWRKIAKDEGAKAFKPGAWNSVLRGMGG-APVLVLYDEIKKY 296  
Db 328 QTYTSVIDCPKILREEGPKALWKAGARVFRSSPQFGVTLLTYELLQRM 378

## RESULT 9

US-09-160-119-2  
; Sequence 2, Application US/09160119A  
; Patent No. 6316219  
; GENERAL INFORMATION:  
; APPLICANT: KRIEF, STEPHANE  
; APPLICANT: SOUCHET, MICHEL  
; APPLICANT: BRIL, ANTOINE  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30985  
; CURRENT APPLICATION NUMBER: US/09/160,119A  
; CURRENT FILING DATE: 1998-09-24  
; EARLIER APPLICATION NUMBER: EP 97402511.6  
; EARLIER FILING DATE: 1997-10-23  
; EARLIER APPLICATION NUMBER: EP 98401655.0  
; EARLIER FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS

US-09-160-119-2

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Best Local Similarity 27.5%; Pred. No. 7.7e-25;
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;

QY 12 FLAGAANAASKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDCVVRIPKEQGLFSFW 71
Db 331 FGLGVAGAGATAVYIDLVKTRMQNRSTGSPVGLMYKNSFDCKFKVLRVYEGFFGLY 390
QY 72 RGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRVYFAGNLASGGAAGATSLCFV 131
Db 391 RGLLPQLLGAPEKAIKLTWDFVRDKFM-----HKDGSVPLAAEILAGCAGGSQVIFT 445
QY 132 YPLDFARTL--AADV--GRRAREFHLGDCIHKFKSDGLRGLYOGFNVSQGIYYR 187
Db 446 NPLEIVKIRIQVAGEITTPRVS-----ALSVDRLGFFGIYKAKACFLRDIPFS 496
QY 188 AAYFGVYDTAKMLPDPKNVHIFVSWIAQSVTAV-AGLLSYDPDVTVRMMQSGKGA 246
Db 497 AIYFPCYAHVKASFANEDGQVSPGSLLAGAIAAGMPAASLVTADVIKTR--LQVAARAG 554
QY 247 DIMYGTGVCWRKIADKDEKAFKFGAWSNVLGMGG-AFVLVLYDEIKKY 296
Db 555 OTTYSVIDCFKILREEGPKALWKAGARVFRSSPQFGVTLTYELLQRW 605

RESULT 10
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501.558
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-501-558-2

Query Match 17.2%; Score 267; DB 4; Length 291;
Best Local Similarity 28.4%; Pred. No. 1.3e-22;
Matches 84; Conservative 51; Mismatches 137; Indels 24; Gaps 9;

QY 10 KDFLAGAANAASKTAVAPIERVKLLQVOHASKQIS-AEKQYKGIIDCVVRIPKEQGL 68
Db 7 KPFVYGLASITAECTGTFIDLVKTRIQIGQNDAKFKRIRYRGMHLVIRIGREGLK 66
QY 69 SPWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRVYFAGNLASGGAAGATSL 128
Db 67 ALYSGIAPAMLRQASGTIKIGIYQSLKRLF---IERPED--ETLPINVICILSGVISS 121
QY 129 CFVYPLDFARTLAADVRRRAQREFHGLGDCIHKFKSDGLRGLYOGFNVSQGIYYRA 188
Db 122 TIANTPTDVLKIRMQA-----QSNTIQGGMIGNFNFIYQOEGTRGLWKGVSILTAQRAAIV 177
QY 189 AAYFGVYDTAK-----GMLPDPKNVHIFVSWIAQSVTAVAG-LLSYDPDVTVRMMQMS 241
Db 178 VELPVDITKHLILSGMGDTVTYTHLSF-----TCGLAGALASNPVDVVRTRMMNOR 232
QY 242 G-RKGADIMYGTGVCWRKIADKDEKAFKFGAWSNVLR-GMGGAFVLVLYDEIKK 295
Db 233 VLDRGRCGGYGTGLDCLLQTKNEGFPALYKGFWPNWLRGLGPNWNIFFITYEQLK 288

RESULT 11
US-09-482-273-118

Sequence 118, Application US/09482273
Patent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 118
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (335)
OTHER INFORMATION: Xaa equals stop translation
US-09-482-273-118

Query Match 17.1%; Score 265.5; DB 4; Length 335;
Best Local Similarity 30.0%; Pred. No. 2.4e-22;
Matches 89; Conservative 43; Mismatches 138; Indels 27; Gaps 10;

QY 10 KDFLAGAANAASKTAVAPIERVKLLQVOHASKQIS- - - - -EKQYKGIIDCVVRIPKEQ 66
Db 51 KPFVYGLASITAECTGTFIDLVKTRIQIGQNDAKFKRIRYRGMHLVIRIGREGLK 108
QY 67 FLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRVYFAGNLASGGAAGAT 126
Db 109 VLALYSGIAPAMLRQASGTIKIGIYQSLKRLF---VERLED--ETLLINMICVVSGVI 163
QY 127 SLCFVYPLDFARTLAADVRRRAQREFHGLGDCIHKFKSDGLRGLYOGFNVSQGIYY 186
Db 164 SSTIANPTDVLKIRMQA--GSLPQSGMIG---SFIDIYQOEGTRGLWKGVSILTAQRAAIV 219
QY 187 RAAFGVYDTAK-----GMLPDPKNVHIFVSWIAQSVTAVAG-LLSYDPDVTVRMM 239
Db 220 VGVLPVYDITKHLILSGMGDTILTH-----FVSSFTCGLAGALASNPVDVVRTRMMN 274
QY 240 QSGRKGADIMYGTGVCWRKIADKDEKAFKFGAWSNVLR-GMGGAFVLVLYDEIKK 295
Db 275 ORAIVGHVDLYKGTVDGILKMWKHEGFPALYKGFWPNWLRGLGPNWNIFFITYEQLK 331

RESULT 12
US-08-933-750C-12
; Sequence 12, Application US/08933750C
; Patent No. 5932442
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
```



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/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/933,750C
/ FILING DATE: September 23, 1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0356 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 320 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: SPLNOT02
/ CLONE: 207452
/
US-08-933-750C-12

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```

Query Match 15.3%; Score 238; DB 2; Length 320;
Best Local Similarity 23.5%; Pred. No. 3.6e-19;
Matches 71; Conservative 67; Mismatches 124; Indels 40; Gaps 10;

QY 13 LAGAVAAAVSKTAVAPIERVKLLQVHAS-KQISAEKQYKGIIDCVRIKPEQGFLSEW 71
DB 20 VAGSVGLVTRALISPFVDIKIRFQLOHERLSRSDPSAKYHGLQASRQILQEGPTAW 79

QY 72 RGNLANVIRYFPTQALNF-AFKDKYKQLFLGGVDRHKQFWRYPAGNLASGGAAGATSLCF 130
DB 80 KGHVPAQILSIGYAGVQFLSFEMLTENVHRSVYDAREFSVHF-----VCGGLAACMATLT 135

QY 131 VYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIHIIYRAAY 190
DB 136 VHPVDVLRTRFAA---QGEPKVYNTLRHAGVTMYRSEGPQVFKYGLAPTLIAIFPYAGLQ 192

QY 191 FGVDYDTAKGMLPDPKKNVHIFVSWMI-----AQSVTAVAGLLSYPPDTVRR 235
DB 193 FSCYSSLK-----HLX-KWAIPEAGKKNENLQNLCCSGAGVISKTLTYPLDLFKK 242

QY 236 RMM-----QSGRK--GADIMYTGTVDCWRKIAKDEGAKAFKPGAWSNVLR-GMGGAFLVL 289
DB 243 RLQVGGFEHARAFAFGVRRYKGLMDCAKQVLOKEGALGFPFKGLSPSLLKAALSTGFMFFS 302

QY 290 YD 291
DB 303 YE 304

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RESULT 13
US-09-234-613-12
/ Sequence 12, Application US/09234613
/ Patent No. 6132973
/ GENERAL INFORMATION:
/ APPLICANT: Lal, Preeti
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Bandman, Olga
/ APPLICANT: Shah, Purvi
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Yue, Henry

```

```

/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
/ NUMBER OF SEQUENCES: 98
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/234,613
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/933,750
/ FILING DATE: September 23, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0356 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 320 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: SPLNOT02
/ CLONE: 207452
/
US-09-234-613-12

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Query Match 15.3%; Score 238; DB 3; Length 320;
Best Local Similarity 23.5%; Pred. No. 3.6e-19;
Matches 71; Conservative 67; Mismatches 124; Indels 40; Gaps 10;

QY 13 LAGAVAAAVSKTAVAPIERVKLLQVHAS-KQISAEKQYKGIIDCVRIKPEQGFLSEW 71
DB 20 VAGSVGLVTRALISPFVDIKIRFQLOHERLSRSDPSAKYHGLQASRQILQEGPTAW 79

QY 72 RGNLANVIRYFPTQALNF-AFKDKYKQLFLGGVDRHKQFWRYPAGNLASGGAAGATSLCF 130
DB 80 KGHVPAQILSIGYAGVQFLSFEMLTENVHRSVYDAREFSVHF-----VCGGLAACMATLT 135

QY 131 VYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIHIIYRAAY 190
DB 136 VHPVDVLRTRFAA---QGEPKVYNTLRHAGVTMYRSEGPQVFKYGLAPTLIAIFPYAGLQ 192

QY 191 FGVDYDTAKGMLPDPKKNVHIFVSWMI-----AQSVTAVAGLLSYPPDTVRR 235
DB 193 FSCYSSLK-----HLX-KWAIPEAGKKNENLQNLCCSGAGVISKTLTYPLDLFKK 242

QY 236 RMM-----QSGRK--GADIMYTGTVDCWRKIAKDEGAKAFKPGAWSNVLR-GMGGAFLVL 289
DB 243 RLQVGGFEHARAFAFGVRRYKGLMDCAKQVLOKEGALGFPFKGLSPSLLKAALSTGFMFFS 302

QY 290 YD 291
DB 303 YE 304

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RESULT 14
US-09-142-565-2

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```

; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; US-09-142-565-2

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```

Query Match      15.0%; Score 233.5; DB 3; Length 312;
Best Local Similarity 24.7%; Pred. No. 1.2e-18;
Matches 73; Conservative 53; Mismatches 145; Indels 25; Gaps 8;

Qy 12 FLAGAVAAVSKTAVAPIERVKLLQVQHASKQISAEK--QYKGIIDCVVRIPKEQGFLS 69
Db 17 FLAGAGTAAACFADLVTFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMTILTWTVEGPR 76
Qy 70 FWRGNLANVIRYPTQALNFAFKDKYKQLFL-GGVDRHKQFWRYPFAGNLASGGAAGATSL 128
Db 77 PYNGLVAGLQRMQSFASIRIGLYDSVKQVTPPKGADNSLTTRILA-----GCTTGAMAV 131
Qy 129 CFVVPDLPFARTLAADV---GRRARQEFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIL 185
Db 132 TCAQPTDVVKVRFOASHLGFPSRDRKYSGTMDAYRTIAREEGVRLWKGTLPNIMRNAI 191
Qy 186 YRAAYFGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTA-----VAGLLSYPPFTVRRRMMQ 240
Db 192 VNCAEVVYDILKEKLLD---YHLLTDFCHPVSFAFGAGFCATVVASPVDVVKTRYM-- 246
Qy 241 SGRKGADIMYTGTVDCWRKIADKDEGAKAFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
Db 247 ---NSPPGQYFSPDLDCMIKMQAEGGTAFYKGFPSFLRLGSLWNVVMFVYEQLR 299

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## RESULT 15

```

US-08-518-878B-56
; Sequence 56, Application US/08518878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518,878B
; FILING DATE: 23-AUG-1995

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-08-518-878B-56

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Query Match      14.6%; Score 227; DB 1; Length 299;
Best Local Similarity 23.8%; Pred. No. 6.2e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

Qy 12 FLAGAVAAVSKTAVAPIERVKLLQVQHASK---QISAEKQYKGIIDCVVRIPKEQGFL 68
Db 7 FLAGAGTAAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMTILTWTVEGPR 66
Qy 69 SFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPFAGNLASGGAAGATSL 128
Db 67 SLYNGLVAGLQRMQSFASVIRIGLYDSVKQVTPPKGSEHAS-----IGSRLLAGSTTGALAV 121
Qy 129 CFVVPDLPFARTLAADV---GRRARQEFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIILYRA 188
Db 122 AVAQPTDVVKVRFOASHLGFPSRDRKYSGTMDAYRTIAREEGVRLWKGTSPNARNAINVC 181
Qy 189 AYFGVYDTAK-----GMLPDPKKNVHIFVSWMIAQSVTAVAGLLSYPPFTVRRRMMQSG 242
Db 182 AELVTVYDILKDALKANLMTDDLPCF-FTSAFGAGFCTTV---IASPVDVVKTRYM--- 233
Qy 243 RKGADIMYTGTVDCWRKIADKDEGAKAFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
Db 234 -NSALQYSSAGHCALTMILQKEGPRAFYKGFMPSPFLRLGSLWNVVMFVYEQLR 286

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Search completed: December 30, 2003, 09:58:01  
Job time : 22 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:57:01 ; Search time 32 Seconds  
(without alignments)  
1847.131 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence:

1 MGDHWSFLKDFLAGAVAA.....LRMGAFVLVLYBIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1553	100.0	297	9	US-09-811-094-31
2	1553	100.0	297	9	US-09-810-644-31
3	1553	100.0	297	10	US-09-185-904A-31
4	1391.5	89.6	298	9	US-09-811-094-32
5	1391.5	89.6	298	9	US-09-810-644-32
6	1391.5	89.6	298	10	US-09-185-904A-32
7	1385.5	89.2	298	9	US-09-811-094-33
8	1385.5	89.2	298	9	US-09-810-644-33
9	1385.5	89.2	298	10	US-09-185-904A-33
10	1045.5	67.3	313	12	US-10-369-493-6072
11	1043.5	67.2	313	12	US-10-369-493-6103
12	1037.5	66.8	300	12	US-10-369-493-5919
13	1005.5	64.7	300	12	US-10-369-493-5088
14	773.5	49.8	179	12	US-10-029-386-32501
15	772	49.7	306	12	US-10-369-493-6116

16	771	49.6	301	12	US-10-032-585-7194	Sequence 7194, Ap
17	752.5	48.5	322	12	US-10-369-493-2374	Sequence 2374, Ap
18	745.5	48.0	326	12	US-10-369-493-6333	Sequence 6333, Ap
19	740	47.6	381	12	US-10-141-478A-2	Sequence 2, Appl
20	736	47.4	307	12	US-10-369-493-1450	Sequence 1450, Ap
21	734	47.3	318	10	US-09-801-368-252	Sequence 252, App
22	734	47.3	318	12	US-10-369-493-1421	Sequence 1421, Ap
23	734	47.3	386	9	US-09-734-569-170	Sequence 170, App
24	718.5	46.3	309	12	US-10-369-493-1876	Sequence 1876, Ap
25	706.5	45.5	368	12	US-10-369-493-4217	Sequence 4217, Ap
26	703.5	45.3	308	15	US-10-128-714-3338	Sequence 3338, Ap
27	703.5	45.3	308	15	US-10-128-714-8338	Sequence 8338, Ap
28	676	43.5	298	12	US-10-369-493-6885	Sequence 6885, Ap
29	666	42.9	677	12	US-10-259-165-192	Sequence 192, App
30	461	29.7	132	9	US-09-925-301-1459	Sequence 1459, Ap
31	433.5	27.9	197	12	US-10-369-493-13335	Sequence 13335, A
32	402.5	25.9	87	9	US-09-864-761-36440	Sequence 36440, A
33	350.5	22.6	475	10	US-09-777-921A-4	Sequence 4, Appl
34	346.5	22.3	477	10	US-09-777-921A-2	Sequence 2, Appl
35	320.5	20.6	384	12	US-10-094-749-1789	Sequence 1789, Ap
36	313	20.2	326	12	US-10-369-493-32510	Sequence 22510, A
37	312	20.1	410	10	US-09-777-921A-5	Sequence 5, Appl
38	306	19.7	680	12	US-10-291-172-339	Sequence 339, App
39	304	19.6	469	9	US-09-989-722-289	Sequence 289, App
40	304	19.6	469	9	US-09-989-723-289	Sequence 289, App
41	304	19.6	469	9	US-09-989-279-289	Sequence 289, App
42	304	19.6	469	9	US-09-989-727-289	Sequence 289, App
43	304	19.6	469	10	US-09-989-731-289	Sequence 289, App
44	304	19.6	469	10	US-09-989-732-289	Sequence 289, App
45	304	19.6	469	10	US-09-991-073-289	Sequence 289, App

#### ALIGNMENTS

#### RESULT 1

US-09-811-094-31

; Sequence 31, Application US/09811094

; Patent No. US20010044144A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Christen M.

; APPLICANT: Davis, Robert E.

; APPLICANT: Clevenger, William

; APPLICANT: Wiley, Sandra Eileen

; APPLICANT: Willer, Scott W.

; APPLICANT: Szabo, Tomas R.

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Moos, Walter H.

; APPLICANT: Pei, Yashong

; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT)

; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

; FILE REFERENCE: 660088.420D4

; CURRENT APPLICATION NUMBER: US/09/811,094

; CURRENT FILING DATE: 2001-03-14

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 31

; LENGTH: 297

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-811-094-31

Query Match 100.0%; Score 1553; DB 9; Length 297;  
Best Local Similarity 100.0%; Pred. No. 2.3e-160;  
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGDHWSFLKDFLAGAVAAVKTAAPVIERVKLLQVHASKQISAEKQYKGIIDCVVR 60

QY 61 IPKEQGFSLFWRGNLANVIRYPTPTALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAG 120

Db 61 IPKEQGFSLFWRGNLANVIRYPTPTALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAG 120

QY 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSV 180  
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 Db 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSV 180  
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 QY 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240  
 |||||  
 Db 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240  
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 QY 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297  
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 Db 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297  
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## RESULT 2

US-09-810-644-31  
 ; Sequence 31, Application US/09810644  
 ; Patent No. US20020012992A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Christen M.  
 ; APPLICANT: Davis, Robert E.  
 ; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Willey, Scott W.  
 ; APPLICANT: Szabo, Tomas R.  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Moos, Walter H.  
 ; APPLICANT: Pei, Yazhong  
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
 ; FILE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
 ; FILE REFERENCE: 660088.420D3  
 ; CURRENT APPLICATION NUMBER: US/09/810,644  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 31  
 ; LENGTH: 297  
 ; TYPE: PR1  
 ; ORGANISM: Homo sapien  
 US-09-810-644-31

Query Match 100.0%; Score 1553; DB 9; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-160;  
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHWSFLKDFLAGAATAVAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60  
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 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLSG 120  
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 Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLSG 120  
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 QY 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSV 180  
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 Db 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSV 180  
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 QY 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240  
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 Db 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240  
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 QY 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297  
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 Db 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297  
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## RESULT 3

US-09-185-904A-31  
 ; Sequence 31, Application US/09185904A  
 ; Patent No. US2002017185A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Christen M.  
 ; APPLICANT: Davis, Robert E.

; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Willey, Scott W.  
 ; APPLICANT: Szabo, Tomas R.  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
 ; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
 ; FILE REFERENCE: 660088.420  
 ; CURRENT APPLICATION NUMBER: US/09/185,904A  
 ; CURRENT FILING DATE: 1998-11-03  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 31  
 ; LENGTH: 297  
 ; TYPE: PR1  
 ; ORGANISM: Homo sapien  
 US-09-185-904A-31

Query Match 100.0%; Score 1553; DB 10; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-160;  
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MGDHWSFLKDFLAGAATAVAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60  
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 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLSG 120  
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 Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLSG 120  
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 QY 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSV 180  
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 Db 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREPHGLGDCIIKIPKSDGLRGLYQGFNVSV 180  
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 QY 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240  
 |||||  
 Db 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240  
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 QY 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297  
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 Db 241 SGRKGADIMYTGTVDCWRKIADGAKAFKPGAWSNVLGRMGAFVLVLYDEIKKYV 297  
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## RESULT 4

US-09-811-094-32  
 ; Sequence 32, Application US/09811094  
 ; Patent No. US20010044144A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Christen M.  
 ; APPLICANT: Davis, Robert E.  
 ; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Willey, Scott W.  
 ; APPLICANT: Szabo, Tomas R.  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Moos, Walter H.  
 ; APPLICANT: Pei, Yazhong  
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
 ; FILE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
 ; FILE REFERENCE: 660088.420D4  
 ; CURRENT APPLICATION NUMBER: US/09/811,094  
 ; CURRENT FILING DATE: 2001-03-14  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 32  
 ; LENGTH: 298  
 ; TYPE: PR1  
 ; ORGANISM: Homo sapien  
 US-09-811-094-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;  
 Best Local Similarity 88.6%; Pred. No. 8.6e-143;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
DB 1 MTDAAISFAKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60  
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120  
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120  
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIPKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIPKSDGLRGLYQGFNVS 180  
QY 180 VQGIITYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSYPPFTVRRMM 239  
DB 181 VQGIITYRAAYFGVYDTAKGMLPDPKNTHIVISWMIATVAVAGLSYPPFTVRRMM 240  
QY 240 QSGRGADIMYTGTDVDCWRKIADGAKAFKPGAWSNVLRGMGGAFVLYLDEIKKY 296  
DB 241 QSGRGADIMYTGTDVDCWRKIADGAKAFKPGAWSNVLRGMGGAFVLYLDEIKKY 297

RESULT 5  
US-09-810-644-32  
; Sequence 32, Application US/09810644  
; Patent No. US20020012992A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Davis, Robert E.  
; APPLICANT: Clevenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Willey, Scott W.  
; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Moos, Walter H.  
; APPLICANT: Pei, Yashong  
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
; FILE REFERENCE: 660088.4203  
; CURRENT APPLICATION NUMBER: US/09/810,644  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-810-644-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;  
Best Local Similarity 88.6%; Pred. No. 8.6e-143;  
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
DB 1 MTDAAISFAKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60  
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120  
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120  
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIPKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIPKSDGLRGLYQGFNVS 180  
QY 180 VQGIITYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSYPPFTVRRMM 239  
DB 181 VQGIITYRAAYFGVYDTAKGMLPDPKNTHIVISWMIATVAVAGLSYPPFTVRRMM 240  
QY 240 QSGRGADIMYTGTDVDCWRKIADGAKAFKPGAWSNVLRGMGGAFVLYLDEIKKY 296  
DB 241 QSGRGADIMYTGTDVDCWRKIADGAKAFKPGAWSNVLRGMGGAFVLYLDEIKKY 297

RESULT 6

US-09-185-904A-32  
; Sequence 32, Application US/09185904A  
; Patent No. US20020177185A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Davis, Robert E.  
; APPLICANT: Clevenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Willey, Scott W.  
; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.  
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
; TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
; FILE REFERENCE: 660088.420  
; CURRENT APPLICATION NUMBER: US/09/185,904A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-185-904A-32

Query Match 89.6%; Score 1391.5; DB 10; Length 298;  
Best Local Similarity 88.6%; Pred. No. 8.6e-143;  
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
DB 1 MTDAAISFAKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60  
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120  
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120  
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIPKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIPKSDGLRGLYQGFNVS 180  
QY 180 VQGIITYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSYPPFTVRRMM 239  
DB 181 VQGIITYRAAYFGVYDTAKGMLPDPKNTHIVISWMIATVAVAGLSYPPFTVRRMM 240  
QY 240 QSGRGADIMYTGTDVDCWRKIADGAKAFKPGAWSNVLRGMGGAFVLYLDEIKKY 296  
DB 241 QSGRGADIMYTGTDVDCWRKIADGAKAFKPGAWSNVLRGMGGAFVLYLDEIKKY 297

RESULT 7

US-09-811-094-33  
; Sequence 33, Application US/09811094  
; Patent No. US20010044144A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Davis, Robert E.  
; APPLICANT: Clevenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Willey, Scott W.  
; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Moos, Walter H.  
; APPLICANT: Pei, Yashong  
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),  
; FILE REFERENCE: 660088.4204  
; CURRENT APPLICATION NUMBER: US/09/811,094  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 37

Query Match 89.6%; Score 1391.5; DB 9; Length 298;  
Best Local Similarity 88.6%; Pred. No. 8.6e-143;  
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
DB 1 MTDAAISFAKDLFLAGVAAVSKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60  
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120  
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLAGS 120  
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIPKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIPKSDGLRGLYQGFNVS 180  
QY 180 VQGIITYRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSYPPFTVRRMM 239  
DB 181 VQGIITYRAAYFGVYDTAKGMLPDPKNTHIVISWMIATVAVAGLSYPPFTVRRMM 240  
QY 240 QSGRGADIMYTGTDVDCWRKIADGAKAFKPGAWSNVLRGMGGAFVLYLDEIKKY 296  
DB 241 QSGRGADIMYTGTDVDCWRKIADGAKAFKPGAWSNVLRGMGGAFVLYLDEIKKY 297



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; TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE:  38-101520521B
; CURRENT APPLICATION NUMBER:  US/10/369,493
; CURRENT FILING DATE:  2003-02-28
; PRIOR APPLICATION NUMBER:  US 60/360,039
; PRIOR FILING DATE:  2002-02-21
; NUMBER OF SEQ ID NOS:  47374
; SEQ ID NO 6072
; LENGTH:  313
; TYPE:  PRT
; ORGANISM:  Caenorhabditis elegans
US-10-369-493-6072

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Query Match	67.3%;	Score 1045.5;	DB 12;	Length 313;
Best Local Similarity	65.8%;	Pred. No. 3.9e+105;		
Matches 203;	Conservative 36;	Mismatches 49;	Indels 3;	Gaps 2;
Qy	8	FLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEQYKGIIDCVVRIPKEQGF	67	
Db	25	FLIDLASGGTAAVASKTAVAPIERVKLLQVODASLTIAADKRYKGIVDLVRVKEQGY	84	
Qy	68	LSFWRGNLNVIRVPTQALNFAFKDYKQFLGQVDRHKQFYEFAGNLASGGAAGTS	127	
Db	85	AAUWRGNLNVIRVPTQALNFAFKDYKQFIQKGLDKKQDFWKFAGNLASGGAAGATS	144	
Qy	128	LCFYVPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIYYR	187	
Db	145	LCFYVPLDFARTRLAADVGRANEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIYYR	204	
Qy	188	AAVFGVYDTAKGML-PPQKNVHIEVSNMIAQSVTTAVAGLLSYPDVTVRRMMQSGRKA	246	
Db	205	AAVFGMEDTAKWVTTADGKLLNFAAWAIAQVTVGSGILSYPDVTVRRMMQSGRR--	262	
Qy	247	DIWYTGTVDCWRKIADDEGAKAFKFGAWSNVLRWGGGAFVLVLVDEIKKYV	297	
Db	263	DVLYKNTLDCAVKIIKNEGASAMFKGALSNVFRGTGALVLAIVDEIQKF	313	

```

RESULT 11
US-10-369-493-6103
; Sequence 6103, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6103
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6103

```

[illegible][illegible]

```

RESULT 12
US-10-369-493-5919
; Sequence 5919, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5919
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5919

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[illegible]

RESULT 13  
US-10-369-493-5088  
; Sequence 5088, Application US/10369493  
; Publication No. US2003023675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 5088

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-5088

Query Match 64.7%; Score 1005.5; DB 12; Length 300;

Best Local Similarity 66.0%; Pred. No. 8.2e-101;

Matches 192; Conservative 40; Mismatches 56; Indels 3; Gaps 2;

QY 8 FLKDFLAGAATAVAVKTAVERVVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGF 67

DB 12 FLVDLASGGTAATKSTAVAPIERVKLLQVSDVSETVADKKYKGMVLAARVPEQGY 71

QY 68 LSWRGNLANVIRYPTQALNFAKPKYKQLFGLGVDRHKQFWRYPAGNLAGGAAGATS 127

DB 72 AAFWRGNLANVIRYPTQALNFAKPKYKQFQEGIDKNEFWKFFAGNLAGGAAGATS 131

QY 128 LCFVPLDFARTLAADVGRRAQREHGLGDCIKIIFKSDGLRGLYQGFNVSVQGI 187

DB 132 LCFVPLDFARTLAADVGRRAQREHGLGDCIKIIFKSDGLRGLYQGFNVSVQGI 191

QY 188 AAYFGVYDVTAKGML-PDPKNVHIFVSMIAQSVTAVAGLLSYFPDVTVRMMQSGRKA 246

DB 192 AAYFGVYDVTAKGML-PDPKNVHIFVSMIAQSVTAVAGLLSYFPDVTVRMMQSGRKA 249

QY 247 DIMYTGTVDCWRKIADDEKAKAFKAGSNVLRGMGAFVLVLYDEIKKYV 297

DB 250 DILYKNTLDCVRKIVKNEGITALYKGLSNVFRATGALVLTIDEIQLHI 300

RESULT 14

US-10-029-386-32501

; Sequence 32501, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 32501

; LENGTH: 179

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC004000.1

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

; OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUATE 2.00e-83

US-10-029-386-32501

Query Match

Best Local Similarity 49.8%; Score 773.5; DB 12; Length 179;

Matches 144; Conservative 12; Mismatches 6; Indels 1; Gaps 1;

QY 38 VQHASQKQISAEKQYKGIIDCVVRIPKEQGFSLFWRGNLANVIRYPTQALNFAKDKYKQ 97

DB 1 VQHASQKQISAEKQYKGIIDCVVRIPKEQGFSLFWRGNLANVIRYPTQALNFAKDKYKQ 60

QY 98 LFLGGVDRHKQFWRYPAGNLAGGAAGATSFCFVPLDFARTLAADVGRRAQREHGL 156

DB 61 IFLGGVDRHKQFWRYPAGNLAGGAAGATSFCFVPLDFARTLAADVGRRAQREHGL 120

QY 157 GDCIKIIFKSDGLRGLYQGFNVSVQGI11YRAAYFGVYDVTAKG 199

DB 121 GDCIKIIFKSDGLRGLYQGFNVSVQGI11YRAAYFGVYDVTAKG 163

RESULT 15

US-10-369-493-6116

; Sequence 6116, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 6116

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-6116

Query Match 49.7%; Score 772; DB 12; Length 306;

Best Local Similarity 51.0%; Pred. No. 2.1e-75;

Matches 150; Conservative 48; Mismatches 90; Indels 6; Gaps 3;

QY 5 AWSFLKDFLAGAATAVAVKTAVERVVKLLQVHASKQISAEKQYKGIIDCVVRIPKE 64

DB 18 AQKFAIDLLIGVSASVSKTVVAPIERVKLLQVSHKDIADKKYNGIIDAFVVRPKE 77

QY 65 QGFLSPWRGNLANVIRYPTQALNFAKPKYKQLFGLGVDRHKQFWRYPAGNLAGGAAG 124

DB 78 QGFLSPWRGNLANVIRYPTQALNFAKPKYKQLFGLGVDRHKQFWRYPAGNLAGGAAG 137

QY 125 ATSLCFVYPLDFARTLAADVGRRAQREHGLGDCIKIIFKSDGLRGLYQGFNVSVQGI 184

DB 138 CSSLCIVYPLDFARTLAADVGRRAQREHGLGDCIKIIFKSDGLRGLYQGFNVSVQGI 197

QY 185 IYRAAYFGVYDVTAKGML-PDPKNVHIFVSMIAQSVTAVAGLLSYFPDVTVRMMQSGR 243

DB 198 IYRSVYFGLYDAIRNTINTDKKLPYASFAIAQGVTLSSVLTYPDVTVRMMQSGR 256

QY 244 KGADIMYTGTVDCWRKIADDEKAKAFKAGSNVLRGMGAFVLVLYDEIKKYV 297

DB 257 LSTSKAFSA-----RKIVHEEGVGRGLYKALANIPRSAGGALVMALEYEIHKHM 306

Search completed: December 30, 2003, 10:02:31

Job time: 33 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 09:51:25 ; Search time 42 Seconds  
(without alignments)  
1122.424 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHWSFLKDLGAVAAA.....LRMGAGFVLVLYDEIKKTV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1553	100.0	297	21	AAU01031 Human adenine nucl
2	1553	100.0	297	22	AAU01198 Human adenine nucl
3	1553	100.0	297	23	AAU10378 Human adenine nucl
4	1357.5	93.9	298	19	AAU61169 Anti protein. Mus
5	1442.5	92.9	293	22	ABU53219 Human metabolism-a
6	1398.5	90.1	298	23	AAU18516 Human insulin rece
7	1391.5	89.6	298	21	AAU71032 Human adenine nucl
8	1391.5	89.6	298	22	AAU01199 Human adenine nucl
9	1391.5	89.6	298	23	AAU10379 Human adenine nucl

10	1385.5	89.2	298	21	AAU71033 Human adenine nucl
11	1385.5	89.2	298	22	AAU39641 Human polypeptide
12	1385.5	89.2	298	22	AAU01200 Human adenine nucl
13	1385.5	89.2	298	23	AAU10380 Human adenine nucl
14	1385.5	89.2	323	22	AAU41427 Human polypeptide
15	1294.5	83.4	325	22	ABG15423 Novel human dieno
16	1268.5	81.7	429	24	ABR41715 Human DITHP organo
17	1241	79.9	299	22	ABR66082 Drosophila melanog
18	1241	79.9	299	22	ABR66082 Drosophila melanog
19	1221.5	78.7	263	22	ABG27056 Novel human dieno
20	1147	73.9	307	22	ABG27056 Drosophila melanog
21	1101.5	70.9	315	22	ABU53218 Human metabolism-a
22	1101.5	70.9	315	23	AAE21175 Human TRICH-19 pro
23	926.5	59.7	228	23	ABP43205 Human ovarian anti
24	867.5	55.9	222	23	ABP74106 Human TRICH SEQ ID
25	820	52.8	298	22	ABG18922 Novel human dieno
26	771	49.6	301	23	ABP73357 Candida albicans e
27	746.5	48.1	379	24	ABP81267 Arabidopsis thalia
28	746	48.0	346	21	AAU36577 Arabidopsis thalia
29	746	48.0	346	21	AAU37261 Arabidopsis thalia
30	746	48.0	346	21	AAU37264 Arabidopsis thalia
31	746	48.0	346	21	AAU38460 Arabidopsis thalia
32	746	48.0	363	21	AAU38576 Arabidopsis thalia
33	746	48.0	363	21	AAU37260 Arabidopsis thalia
34	746	48.0	363	21	AAU37263 Arabidopsis thalia
35	746	48.0	363	21	AAU38459 Arabidopsis thalia
36	746	48.0	381	21	AAU36575 Arabidopsis thalia
37	746	48.0	381	21	AAU37259 Arabidopsis thalia
38	746	48.0	381	21	AAU37262 Arabidopsis thalia
39	746	48.0	381	21	AAU38458 Arabidopsis thalia
40	746	48.0	992	21	AAU38672 Arabidopsis thalia
41	746	48.0	1009	21	AAU38671 Arabidopsis thalia
42	746	48.0	1027	21	AAU38670 Arabidopsis thalia
43	743	47.8	346	21	AAU17731 Arabidopsis thalia
44	743	47.8	363	21	AAU17730 Arabidopsis thalia
45	743	47.8	381	21	AAU17729 Arabidopsis thalia

#### ALIGNMENTS

RESULT 1

AAU71031

ID AAU71031 standard; Protein; 297 AA.

XX AAU71031;

AC AAU71031;

XX 29-AUG-2000 (first entry)

DT Human adenine nucleotide translocator ANTI.

DE Human; adenine nucleotide translocator; ANTI; mitochondria; ADP; ATP;

KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
KW mitochondrial permeability transition; neuroprotective; nontropic;  
KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
KW antipsoriatic; cerebroprotective; therapeutic; psoriasis;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
KW myoclonic epilepsy red ragged fibre syndrome.

OS Homo sapiens.

XX WO200026370-A2.

PN 11-MAY-2000.

XX 03-NOV-1999; 99WO-US25983.

PF 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

XX

PA (MITO-) MITOKOR.  
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
PI Ghosh SS;  
XX WPI; 2000-365619/31.  
XX N-PSDB; AAD00519.  
XX Recombinant construct encoding adenine nucleotide translocator  
PT polypeptide, useful e.g. in screening for potential therapeutic agents  
PT against mitochondrial disease -  
XX  
XX Claim 44; Page 172; 175pp; English.  
XX  
XX The patent discloses a method to produce adenine nucleotide translocator  
CC (ANT) proteins or ANT fusion proteins using recombinant expression  
CC constructs. ANT is a nuclear encoded protein and a major component of  
CC inner mitochondrial membrane. It mediates transport of adenosine  
CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
CC as an important molecular component of the mitochondrial permeability  
CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
CC or ligands that bind to, or interact with it. The ANT ligands are used to  
CC detect or isolate ANT in a biological sample, and therapeutically for  
CC regulating mitochondrial pore activity, for treating diseases associated  
CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia  
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
CC encephalopathy, lactic acidosis and stroke (MLAS), hyperproliferative  
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
CC epilepsy red ragged fibre syndrome. The present sequence is an  
CC adenine nucleotide translocator ANT1 from human brain.  
XX  
XX Sequence 297 AA;  
XX  
XX Query Match 100.0%; Score 1553; DB 21; Length 297;  
XX Best Local Similarity 100.0%; Pred. No. 3.4e-173;  
XX Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGDHWSFLKDFLAGAATAVAPITVIRVLLQVHASKQISAEKQYKGIIDCVVR 60  
Db 1 MGDHWSFLKDFLAGAATAVAPITVIRVLLQVHASKQISAEKQYKGIIDCVVR 60  
Qy 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
Qy 121 GAAGATSLCFVYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
Db 121 GAAGATSLCFVYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
Qy 181 OGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMMNQ 240  
Db 181 OGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMMNQ 240  
Qy 241 SGRKGADIMYTGTVDCWRKIADDEGAKAFKAGNSVLRGMGGAFLVLYDEIKKYV 297  
Db 241 SGRKGADIMYTGTVDCWRKIADDEGAKAFKAGNSVLRGMGGAFLVLYDEIKKYV 297  
RESULT 2  
AAU01198  
ID AAU01198 standard; Protein; 297 AA.  
XX  
XX AAU01198;  
XX  
XX 07-SEP-2001 (first entry)  
XX  
XX Human adenine nucleotide translocator-1 (ANT-1) protein.  
XX  
XX Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;  
XX mitochondrial permeability transition pore component; cell survival;  
XX mitochondrial core component; mitochondrial related disorder; cancer;  
XX Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX OS Homo sapiens.  
XX WO200132876-A2.  
XX 10-MAY-2001.  
XX 03-NOV-2000; 2000WO-US30535.  
XX 03-NOV-1999; 99US-0434354.  
XX (MITO-) MITOKOR.  
XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;  
XX Velicelebi G, Davis RE;  
XX WPI; 2001-291054/30.  
XX N-PSDB; AAS05901.  
XX New nucleic acid expression constructs, useful for screening for agents  
PT that alter mitochondrial permeability transition (MPT), comprises  
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
PT fused to energy transfer molecule -  
XX  
XX Disclosure; Fig 2; 186pp; English.  
XX  
XX The present sequence represents human adenine nucleotide translocator-1  
CC (ANT-1) protein. ANT proteins are mitochondrial permeability  
CC transition (MPT) pore components responsible for mediating transport  
CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
CC with other mitochondrial core components e.g. cyclophilins to  
CC regulate MPT. The present invention relates to a novel nucleic acid  
CC expression construct comprising a promoter operably linked to a  
CC polynucleotide encoding a mitochondrial pore component polypeptide  
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel  
CC expression construct can alter mitochondrial membrane permeability  
CC transition and/or alter the interaction between mitochondrial core  
CC components. The methods are useful for screening for agents that alter  
CC MPT and/or cell survival. These agents are useful for the prevention or  
CC treatment of diseases associated with altered mitochondrial function or  
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
CC mitochondrial encephalopathy, lactic acidosis, stroke,  
CC hyperproliferative disorders e.g. cancer, and deafness.  
XX  
XX Sequence 297 AA;  
XX  
XX Query Match 100.0%; Score 1553; DB 22; Length 297;  
XX Best Local Similarity 100.0%; Pred. No. 3.4e-173;  
XX Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGDHWSFLKDFLAGAATAVAPITVIRVLLQVHASKQISAEKQYKGIIDCVVR 60  
Db 1 MGDHWSFLKDFLAGAATAVAPITVIRVLLQVHASKQISAEKQYKGIIDCVVR 60  
Qy 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
Qy 121 GAAGATSLCFVYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
Db 121 GAAGATSLCFVYPLDFARTLADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
Qy 181 OGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMMNQ 240  
Db 181 OGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMMNQ 240  
Qy 241 SGRKGADIMYTGTVDCWRKIADDEGAKAFKAGNSVLRGMGGAFLVLYDEIKKYV 297  
Db 241 SGRKGADIMYTGTVDCWRKIADDEGAKAFKAGNSVLRGMGGAFLVLYDEIKKYV 297

## RESULT 3

AAU10378  
ID AAU10378 standard; Protein; 297 AA.

AC AAU10378;

XX 14-FEB-2002 (first entry)

DT Human adenine nucleotide translocator 1 (ANT1).

XX Human; adenine nucleotide translocator; ANT;

KW mitochondrial matrix protein.

XX Homo sapiens.

OS WC200185944-A2.

PN 15-NOV-2001.

PD 11-MAY-2001; 2001WO-US15416.

XX 11-MAY-2000; 2000US-0569337.

PR (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;

PI Ghosh SS, Moos WH, Pei Y, Carroll AK;

XX WPI; 2002-055598/07.

DR N-PSDB; AAS16688.

XX Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide

PS Claim 44; Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. CC The present sequence represents the amino acid sequence of human ANT1.

XX Sequence 297 AA;

Query Match 100.0%; Score 1553; DB 23; Length 297;

Best Local Similarity 100.0%; Pred. No. 3.4e-173;

Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHWSFLKDFLAGA VAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60

DB 1 MGDHWSFLKDFLAGA VAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60

QY 61 IPKEQGLSFWRGNLNVIRYFPTQALNFAFKDKYKQLFLGGVDRHRKQFWRYFAGNLASG 120

DB 61 IPKEQGLSFWRGNLNVIRYFPTQALNFAFKDKYKQLFLGGVDRHRKQFWRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIHKIPKSGDLRGLYQGFNVSV 180

DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIHKIPKSGDLRGLYQGFNVSV 180

QY 181 QGIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLSYFPDVTVRRRMMQ 240  
DB 181 QGIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLSYFPDVTVRRRMMQ 240  
QY 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFPKGANSNVLKRGMGAFVLVLYDEIKKYV 297  
DB 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFPKGANSNVLKRGMGAFVLVLYDEIKKYV 297

## RESULT 4

AAW61169

ID AAW61169 standard; Protein; 298 AA.

XX AAW61169;

AC 28-SEP-1998 (first entry)

DT Ant1 protein.

XX Ant1; Adenine nucleotide translocator; cloning; screening;

KW DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;

XX probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;

XX hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;

XX lactic acidosis; degenerative muscle disease.

XX Mus sp.

XX WO9819714-A1.

XX 14-MAY-1998.

XX 31-OCT-1997; 97WO-US19882.

XX 01-NOV-1996; 96US-0030017.

XX (UYEM-) UNIV EMORY.

XX Graham BC, Macgregor GR, Wallace DC;

XX WPI; 1998-286608/25.

XX N-PSDB; AAV36479.

XX Mice lacking heart-muscle adenine nucleotide translocator protein - useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or gene therapies

PS Disclosure; Page 39-40; 61pp; English.

XX The present sequence is the mouse Ant1 protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA Tag dideoxy terminator cycle sequencing. The Ant1 protein is encoded by the Ant1 locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Ant1 homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Ant1 homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane independent of ANT1.

XX Sequence 298 AA;

Query Match 93.9%; Score 1457.5; DB 19; Length 298;

Best Local Similarity 93.6%; Pred. No. 5.4e-162;

Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGA VAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60

DB 1 MGDHWSFLKDFLAGA VAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60

QY 61 IPKEQFLSWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
 DB 61 IPKEQFLSWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSV 179  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
 QY 180 VQGIIRAAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYPPFDTVRBRMM 239  
 DB 181 VQGIIRAAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYPPFDTVRBRMM 240  
 QY 240 QSGRKGADIMYTGTCWRKRIADKGAFFKGAWSNVLRGMCAGFVLYLYDEIKKYV 297  
 DB 241 QSGRKGADIMYTGTCWRKRIADKGAFFKGAWSNVLRGMCAGFVLYLYDEIKKYV 298

RESULT 5  
 ABUS3219  
 ID ABUS3219 standard; Protein; 293 AA.  
 XX  
 AC ABUS3219;  
 XX  
 DT 14-APR-2003 (first entry)  
 XX  
 DE Human metabolism-associated DKFphtes3\_35n12 homologue #1.  
 XX  
 KW Human; gene therapy; vaccine; disease treatment; detection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200112659-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-1B01496.  
 XX  
 PR 18-AUG-1999; 99US-0149499.  
 PR 28-SEP-1999; 99US-0156503.  
 XX  
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
 XX  
 PI Wiemann S;  
 XX  
 DR WPI; 2001-327840/34.  
 XX  
 PT Nucleic acids having the sequences of clones isolated from libraries of  
 different human tissues, useful in recombinant DNA methodologies -  
 XX  
 PS Example III; Page 850; 1095pp; English.  
 CC  
 CC This invention describes novel polynucleotides and polypeptides isolated  
 from human cDNA libraries which can be used for gene therapy or in  
 CC vaccines. The polynucleotides of the invention and antibodies encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate polypeptide expression. The products of the  
 CC invention may also be used to identify modulators of expression and  
 CC activity and to down regulate expression and activity. The antibodies of  
 CC the invention may also be used as diagnostic agents for detecting the  
 CC presence of polypeptides in samples. This sequence represents a homologue  
 CC of a polypeptide described in the disclosure of the invention.  
 XX  
 SQ Sequence 293 AA;

Query Match 92.9%; Score 1442.5; DB 22; Length 293;  
 Best Local Similarity 94.2%; Pred. No. 3e-160;  
 Matches 276; Conservative 10; Mismatches 6; Indels 1; Gaps 1;  
 QY 5 AWSFLKDFLAGAATAAVSVTAVAPIERVKLLQVQHASKQISAEKQYKGLIDCVRIKPE 64  
 DB 1 ALSFLKDFLAGGATAAVSVTAVAPIERVKLLQVQHASKQISAEKQYKGLIDCVRIKPE 60

QY 65 QGFLSWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASGAG 124  
 DB 61 QGFLSWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASGAG 120  
 QY 125 ATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSVQGI 183  
 DB 121 ATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSVQGI 180  
 QY 184 IYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYPPFDTVRBRMMQSGR 243  
 DB 181 IYRAAYFGVYDTAKGMLPDPKKNVHIFVSWMTAQSVTAVAGLLSYPPFDTVRBRMMQSGR 240  
 QY 244 KGADIMYTGTCWRKRIADKGAFFKGAWSNVLRGMCAGFVLYLYDEIKKY 296  
 DB 241 KGADIMYTGTCWRKRIADKGAFFKGAWSNVLRGMCAGFVLYLYDEIKKY 293

RESULT 6  
 AAO18516  
 ID AAO18516 standard; Protein; 298 AA.  
 XX  
 AC AAO18516;  
 XX  
 DT 11-OCT-2002 (first entry)  
 XX  
 DE Human insulin receptor signaling modifier SEQ ID NO: 54.  
 XX  
 KW Human; insulin receptor signaling; insulin receptor signaling modifier;  
 KW ISM; diabetes; metabolic syndrome; antidiabetic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200255664-A2.  
 XX  
 PD 18-JUL-2002.  
 XX  
 PF 11-JAN-2002; 2002WO-US01048.  
 XX  
 PR 12-JAN-2001; 2001US-261226P.  
 PR 12-JAN-2001; 2001US-261303P.  
 PR 12-JAN-2001; 2001US-261304P.  
 PR 12-JAN-2001; 2001US-261335P.  
 PR 12-JAN-2001; 2001US-261366P.  
 PR 12-JAN-2001; 2001US-261361P.  
 PR 12-JAN-2001; 2001US-261456P.  
 PR 12-JAN-2001; 2001US-261457P.  
 PR 12-JAN-2001; 2001US-261458P.  
 PR 12-JAN-2001; 2001US-261459P.  
 PR 12-JAN-2001; 2001US-261461P.  
 PR 12-JAN-2001; 2001US-261518P.  
 PR 12-JAN-2001; 2001US-261531P.  
 PR 12-JAN-2001; 2001US-261532P.  
 PR 12-JAN-2001; 2001US-261589P.  
 PR 12-JAN-2001; 2001US-261590P.  
 PR 12-JAN-2001; 2001US-261694P.  
 PR 12-JAN-2001; 2001US-261695P.  
 PR 12-JAN-2001; 2001US-261697P.  
 XX  
 PA (EXEL-) EXELIXIS INC.  
 XX  
 PI Seidel-Dugan C, Ferguson KC, Kidd T;  
 XX  
 DR WPI; 2002-599664/64.  
 DR N-PSDB; AAL48635.  
 XX  
 PT Identifying an insulin receptor signaling modulator, useful as drug  
 PT targets for treating diabetes or metabolic disorders, comprises  
 PT contacting an assay system comprising insulin receptor signaling  
 PT modifiers with a test agent -  
 XX  
 PS Disclosure; Page 160-161; 232pp; English.  
 XX  
 CC The present invention relates to a method of identifying a candidate

CC insulin receptor (INR) signaling modulating agent, involving contacting  
 CC an assay system comprising an insulin receptor signaling modifier (ISM)  
 CC polypeptide or nucleic acid with a test agent, and detecting a test  
 CC agent-biased activity of the assay system. The method is useful for  
 CC identifying candidate INR signaling modulating agents. ISM genes may be  
 CC used as drug targets for treatment of disorders related to INR signaling  
 CC such as diabetes or metabolic syndrome. ISM nucleic acids and  
 CC polypeptides are useful for identifying and testing agents that modulate  
 CC INR function and for other applications related to the involvement of ISM  
 CC in INR signaling, and for identifying subjects having a predisposition to  
 CC such diseases associated with INR signaling. The present sequence is an  
 CC ISM protein described in the exemplification of the invention.

XX SQ Sequence 298 AA;  
 CC Query Match 90.1%; Score 1398.5; DB 23; Length 298;  
 CC Best Local Similarity 88.9%; Pred. No. 4.5e-155;  
 CC Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;  
 QY 1 MGDHMSFLKDFLAGAATAVAPVPIRVKLLQVHASKQISAEKQYKGIIDCVVR 60  
 DB 1 MTDAAVSFAKDFLAGGVAATAVAPVPIRVKLLQVHASKQITADKQYKGIIDCVVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKYKQIFLGVDVDRHKQFWRYPAGNLAG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKYKQIFLGVDVDRHKQFWRYPAGNLAG 120  
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREPHGLGDCIIKIFKSDGLRGLYQGPNVS 179  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREPHGLGDCIIKIFKSDGLRGLYQGPNVS 180  
 QY 180 VQGIIRYAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSYFPDTRRRMM 239  
 DB 181 VQGIIRYAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSYFPDTRRRMM 240  
 QY 240 QSGRKGADIMYTGTCVDCWRKIADGAKAPFKGAWSNVLRGMGGAFVLVLYDEIKKY 296  
 DB 241 QSGRKGTDIMYTGTCVDCWRKIADGAKAPFKGAWSNVLRGMGGAFVLVLYDEIKKY 297

RESULT 7  
 AAAY71032  
 ID AAAY71032 standard; Protein; 298 AA.  
 XX  
 AC AAAY71032;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Human adenine nucleotide translocator ANT2.  
 XX  
 KW Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;  
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
 KW mitochondrial permeability transition; neuroprotective; neurotropic;  
 KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
 KW antiporotic; cerebroprotective; therapeutic; screening; psoriasis;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
 KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.  
 XX  
 XX WO200026370-A2.  
 XX  
 PD 11-MAY-2000.  
 XX  
 XX 03-NOV-1999; 99WO-US25883.  
 XX  
 XX 03-NOV-1998; 98US-0185904.  
 PR 08-SEP-1999; 99US-0393441.  
 XX  
 PA (MITO-) MITOKOR.

XX  
 PI Anderson CM, Davies RE, Clevenger W, Willey SE, Miller SW, Szabo TR;  
 Gosh SS;  
 XX  
 DR WPI; 2000-365619/31.  
 DR N-PSDB; AAD00520.  
 XX  
 PT Recombinant construct encoding adenine nucleotide translocator  
 PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 PT against mitochondrial disease  
 XX  
 XX Claim 45; Page 172-173; 175pp; English.

XX The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANT2 from human brain.

XX SQ Sequence 298 AA;

Query Match 89.6%; Score 1391.5; DB 21; Length 298;  
 Best Local Similarity 88.8%; Pred. No. 3e-154;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAATAVAPVPIRVKLLQVHASKQISAEKQYKGIIDCVVR 60  
 DB 1 MTDAAVSFAKDFLAGGVAATAVAPVPIRVKLLQVHASKQITADKQYKGIIDCVVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKYKQIFLGVDVDRHKQFWRYPAGNLAG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKYKQIFLGVDVDRHKQFWRYPAGNLAG 120  
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREPHGLGDCIIKIFKSDGLRGLYQGPNVS 179  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AOREPHGLGDCIIKIFKSDGLRGLYQGPNVS 180  
 QY 180 VQGIIRYAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSYFPDTRRRMM 239  
 DB 181 VQGIIRYAAVFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLSYFPDTRRRMM 240  
 QY 240 QSGRKGADIMYTGTCVDCWRKIADGAKAPFKGAWSNVLRGMGGAFVLVLYDEIKKY 296  
 DB 241 QSGRKGTDIMYTGTCVDCWRKIADGAKAPFKGAWSNVLRGMGGAFVLVLYDEIKKY 297

RESULT 8  
 AAU01199  
 ID AAU01199 standard; Protein; 298 AA.  
 XX  
 AC AAU01199;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.

XX Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.  
 XX

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OS Homo sapiens.
XX WO200132876-A2.
XX 10-MAY-2001.
XX 03-NOV-2000; 2000WO-US30535.
XX 03-NOV-1999; 99US-0434354.
XX (MITO-) MITOKOR.
XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
XX Velicelebi G, Davis RE;
XX WPI; 2001-291054/30.
XX N-PSDB; AAS05902.
XX
XX New nucleic acid expression constructs, useful for screening for agents
XX PT that alter mitochondrial permeability transition (MPT), comprises
XX PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
XX PT fused to energy transfer molecule -
XX
XX Disclosure; Fig 2; 186pp; English.
XX
XX The present sequence represents human adenine nucleotide translocator-2
XX (ANT-2) protein. ANT proteins are mitochondrial permeability
XX transition (MTP) pore components responsible for mediating transport
XX of ADP across the mitochondrial inner membrane. ANT proteins interact
XX with other mitochondrial core components e.g. cyclophilins to
XX regulate MPT. The present invention relates to a novel nucleic acid
XX expression construct comprising a promoter operably linked to a
XX polynucleotide encoding a mitochondrial pore component polypeptide
XX (e.g. ANT) fused to an energy transfer molecule (ETM) protein
XX (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
XX expression construct can alter mitochondrial membrane permeability
XX transition and/or alter the interaction between mitochondrial core
XX components. The methods are useful for screening for agents that alter
XX MPT and/or cell survival. These agents are useful for the prevention or
XX treatment of diseases associated with altered mitochondrial function or
XX dysfunctional cell survival, such as Alzheimer's disease, diabetes
XX mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
XX mitochondrial encephalopathy, lactic acidosis, stroke,
XX hyperproliferative disorders e.g. cancer, and deafness.
XX
XX Sequence 298 AA;
XX
Query Match 89.6%; Score 1391.5; DB 22; Length 298;
Best Local Similarity 88.6%; Pred. No. 3e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHAWFLKDFLAGAFAAASVTAVPIERVKLLQVQHASQKQISAEKQYKGIIDCVVR 60
DB 1 MTDAAISFAKDFLAGGVAASISKTAVAPIERVKLLQVQHASQKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGQVDRHKQFWRYPAGNLASG 120
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNV 180
QY 180 VQGIIRYRAAYFGYDTAKGMLPDPKPNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239
DB 181 VQGIIRYRAAYFGYDTAKGMLPDPKPNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIADEGAKAFKFGAWSNVLRGMGSAFVLVLYDEIKY 296
DB 241 QSGRKGADIMYTGTVDCWRKIADEGAKAFKFGAWSNVLRGMGSAFVLVLYDEIKY 297
XX
XX RESULT 9

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AAU10379
ID AAU10379 standard; Protein; 298 AA.
XX
XX AAU10379;
XX
XX 14-FEB-2002 (first entry)
XX
XX Human adenine nucleotide translocator 2 (ANT2).
XX
XX Human; adenine nucleotide translocator; ANT; ss;
XX KW mitochondrial matrix protein.
XX
XX Homo sapiens.
XX
XX WO200185944-A2.
XX
XX 15-NOV-2001.
XX
XX 11-MAY-2001; 2001WO-US15416.
XX
XX 11-MAY-2000; 2000US-0569327.
XX
XX (MITO-) MITOKOR.
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
XX Chosh SS, Moos WH, Pei Y, Carroll AK;
XX WPI; 2002-055598/07.
XX N-PSDB; AAS16689.
XX
XX Novel recombinant expression construct for producing adenine nucleotide
XX translocator polypeptides, comprises a regulated promoter linked to
XX nucleic acid encoding the polypeptide -
XX
XX Claim 44; Fig 2; 147pp; English.
XX
XX The invention relates to a recombinant expression construct (I)
XX comprising a regulated promoter operably linked to a nucleic acid
XX encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
XX proteins mediate the exchange of ADP synthesised in the mitochondrial
XX matrix for ADP in the cytosol. (I) is useful for producing recombinant
XX ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
XX culturing the host cell. (I) is also useful for targeting a polypeptide
XX of interest to a mitochondrial membrane, where ANT polypeptide is
XX expressed as a fusion protein with the polypeptide of interest.
XX Recombinant ANT polypeptide, or cells expressing the polypeptide, is
XX useful for identifying an agent that binds to an ANT polypeptide. ANT
XX ligand is useful for determining the presence of an ANT polypeptide,
XX preferably ANTI, ANT2 or ANT3 in a biological sample and for isolating
XX ANT from a biological sample, where the ANT ligand is covalently or non-
XX covalently bound to a solid phase. Detectably labeled ANT ligand is also
XX useful for identifying an agent that interacts with an ANT polypeptide.
XX The present sequence represents the amino acid sequence of human ANT2.
XX
XX Sequence 298 AA;
XX
Query Match 89.6%; Score 1391.5; DB 23; Length 298;
Best Local Similarity 88.6%; Pred. No. 3e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHAWFLKDFLAGAFAAASVTAVPIERVKLLQVQHASQKQISAEKQYKGIIDCVVR 60
DB 1 MTDAAISFAKDFLAGGVAASISKTAVAPIERVKLLQVQHASQKQITADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGQVDRHKQFWRYPAGNLASG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGQVDRHKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNV 180
QY 180 VQGIIRYRAAYFGYDTAKGMLPDPKPNVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239

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Db 181 VQGIIRYAAFGIYDTAKGMLPDPKNTHTIVISWMIATQVTAAGLTSYFPDTRRRMM 240  
QY 240 QSGRGADIMYTGTDWCKIAKDECAKAFKAGNSVLRGMGAFVLYLYDEIKKY 296  
Db 241 QSGRGKTDIMYTGTDWCKIAKDEGKAFKAGNSVLRGMGAFVLYLYDEIKKY 297  
RESULT 10  
AAV71033  
ID AAY71033 standard; Protein; 298 AA.  
XX AAY71033;  
XX  
DT 29-AUG-2000 (first entry)  
DE Human adenine nucleotide translocator ANT3.  
XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;  
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
KW mitochondrial permeability transition; neuroprotective; nontropic;  
KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dysconia;  
KW diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;  
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
KW myoclonic epilepsy red ragged fibre syndrome.  
XX Homo sapiens.  
OS  
PN WO200026370-A2.  
XX  
PD 11-MAY-2000.  
XX  
PF 03-NOV-1999; 99WO-US25883.  
XX  
PR 03-NOV-1998; 98US-0185904.  
PR 08-SEP-1999; 99US-0393441.  
XX  
PA (MITO-) MITOKOR.  
XX  
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
PI Ghosh SS;  
PI  
DR WPI: 2000-365619/31.  
DR N-PSDB; AAD00521.  
XX  
PT Recombinant construct encoding adenine nucleotide translocator  
PT polypeptide, useful e.g. in screening for potential therapeutic agents  
PT against mitochondrial disease -  
XX  
XX Claim 46; Page 173-174; 175pp; English.  
PS  
XX The patent discloses a method to produce adenine nucleotide translocator  
CC (ANT) proteins or ANT fusion proteins using recombinant expression  
CC constructs. ANT is a nuclear encoded protein and a major component of  
CC inner mitochondrial membrane. It mediates transport of adenosine  
CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
CC as an important molecular component of the mitochondrial permeability  
CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
CC or ligands that bind to, or interact with it. The ANT ligands are used to  
CC detect or isolate ANT in a biological sample, and therapeutically for  
CC regulating mitochondrial pore activity, for treating diseases associated  
CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
CC epilepsy red ragged fibre syndrome. The present sequence is an  
CC adenine nucleotide translocator ANT3 from human brain.  
XX  
SQ Sequence 298 AA;

Query Match c89.2%; Score 1385.5; DB 21; Length 298;  
Best Local Similarity .87.2%; Pred. No. 1.5e-153;  
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;  
QY 1 MGDHAWSEKDFLAGAVAAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60  
Db 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLQVQHASKQIAADKQYKGIIDCVR 60  
QY 61 IPKEQGLSFWRGNLANVIRYFPTQALNPAKDKYKQLPLGGVDHRKOPWRYFAGNLASG 120  
Db 61 IPKEQGLSFWRGNLANVIRYFPTQALNPAKDKYKQLPLGGVDHRKOPWRYFAGNLASG 120  
QY 121 GAAGATSLCFVYVPLDFARTRLAADVGR- AQREPHGLGDCIIKIPKSDGLRGLYQGFNVS 179  
Db 121 GAAGATSLCFVYVPLDFARTRLAADVGR- AQREPHGLGDCIIKIPKSDGLRGLYQGFNVS 180  
QY 180 VQGIIRYAAFGIYDTAKGMLPDPKNTHTIVISWMIATQVTAAGLTSYFPDTRRRMM 239  
Db 181 VQGIIRYAAFGIYDTAKGMLPDPKNTHTIVISWMIATQVTAAGLTSYFPDTRRRMM 240  
QY 240 QSGRGADIMYTGTDWCKIAKDEGKAFKAGNSVLRGMGAFVLYLYDEIKKY 297  
Db 241 QSGRGADIMYTGTDWCKIAKDEGKAFKAGNSVLRGMGAFVLYLYDEIKKY 298  
RESULT 11  
AAM39641  
ID AAM39641 standard; Protein; 298 AA.  
XX AAM39641;  
XX  
DT 22-OCT-2001 (first entry)  
DE Human polypeptide SEQ ID NO 2786.  
XX  
KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemoknetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX Homo sapiens.  
OS  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US34263.  
XX  
PR 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX (HYSE-) HYSEQ INC.  
PA  
XX Tang YT, Liu C, Aeundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX WPI: 2001-442253/47.  
DR N-PSDB; AAI58797.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -  
XX  
PS Example 4; SEQ ID NO 2786; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AA38642-AA42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX  
 SQ Sequence 298 AA;  
 Query Match 89.2%; Score 1385.5; DB 22; Length 298;  
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 MGDHWSFLKDFLAGAFAAASKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
 DB 1 MTEQAISFAKDFLAGGIAAISKTAVERVKLLQVHASKQIAADKQYKGIIDCVVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180  
 QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYPPFTVRRMM 239  
 DB 181 VQGIILYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQSVTAAGVVSYPFTVRRMM 240  
 QY 240 QSGRGKADIMYTGTVDCWRKIAKDEGAKAFKAGNSVLRGMGGAFLVLYDEIKKYV 297  
 DB 241 QSGRGKADIMYTGTVDCWRKIFRDEGKAFKAGNSVLRGMGGAFLVLYDELKKVI 298  
 RESULT 12  
 AAU01200  
 ID AAU01200 standard; Protein; 298 AA.  
 XX  
 AC AAU01200;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.  
 XX  
 KW Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200132876-A2.  
 XX  
 XX 10-MAY-2001.  
 PD  
 XX  
 PF 03-NOV-2000; 2000WO-US30535.  
 XX  
 PR 03-NOV-1999; 99US-0434354.  
 XX  
 PA (MITO-) MITOKOR.  
 XX  
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;

PI Velicelebi G, Davis RE;  
 XX  
 DR WPI; 2001-291054/30.  
 DR N-PSDB; AAS05903.  
 XX  
 XX New nucleic acid expression constructs, useful for screening for agents  
 XX that alter mitochondrial permeability transition (MPT), comprises  
 XX polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 XX fused to energy transfer molecule -  
 XX  
 PS Disclosure; Fig 2; 186pp; English.  
 XX  
 XX The present sequence represents human adenine nucleotide translocator-3  
 XX (ANT-3) protein. ANT proteins are mitochondrial permeability  
 XX transition (MPT) pore components responsible for mediating transport  
 XX of ADP across the mitochondrial inner membrane. ANT proteins interact  
 XX with other mitochondrial core components e.g. cyclophilins to  
 XX regulate MPT. The present invention relates to a novel nucleic acid  
 XX expression construct comprising a promoter operably linked to a  
 XX polynucleotide encoding a mitochondrial pore component polypeptide  
 XX (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 XX (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel  
 XX expression construct can alter mitochondrial membrane permeability  
 XX transition and/or alter the interaction between mitochondrial core  
 XX components. The methods are useful for screening for agents that alter  
 XX MPT and/or cell survival. These agents are useful for the prevention or  
 XX treatment of diseases associated with altered mitochondrial function or  
 XX dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 XX mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 XX mitochondrial encephalopathy, lactic acidosis, stroke,  
 XX hyperproliferative disorders e.g. cancer, and deafness.  
 XX  
 SQ Sequence 298 AA;  
 Query Match 89.2%; Score 1385.5; DB 22; Length 298;  
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 MGDHWSFLKDFLAGAFAAASKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
 DB 1 MTEQAISFAKDFLAGGIAAISKTAVERVKLLQVHASKQIAADKQYKGIIDCVVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 180  
 QY 180 VQGIILYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYPPFTVRRMM 239  
 DB 181 VQGIILYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQSVTAAGVVSYPFTVRRMM 240  
 QY 240 QSGRGKADIMYTGTVDCWRKIAKDEGAKAFKAGNSVLRGMGGAFLVLYDEIKKYV 297  
 DB 241 QSGRGKADIMYTGTVDCWRKIFRDEGKAFKAGNSVLRGMGGAFLVLYDELKKVI 298  
 RESULT 13  
 AAU10380  
 ID AAU10380 standard; Protein; 298 AA.  
 XX  
 AC AAU10380;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Human adenine nucleotide translocator 3 (ANT3).  
 XX  
 KW Human; adenine nucleotide translocator; ANT;  
 KW mitochondrial matrix protein.  
 XX  
 OS Homo sapiens.



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XX PN WO200185944-A2.
XX PD 15-NOV-2001.
XX PF 11-MAY-2001; 2001WO-US15416.
XX PR 11-MAY-2000; 2000US-0569327.
XX PA (MITO-) MITOKOR.
XX PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
XX DR WPI; 2002-055598/07.
XX DR N-PSDB; AAS16690.
XX PT Novel recombinant expression construct for producing adenine nucleotide
XX FT translocator polypeptides, comprises a regulated promoter linked to
XX FT nucleic acid encoding the polypeptide.
XX PS Example 3; Fig 2; 147pp; English.
XX CC The invention relates to a recombinant expression construct (I)
XX CC comprising a regulated promoter operably linked to a nucleic acid
XX CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
XX CC proteins mediate the exchange of ATP synthesised in the mitochondrial
XX CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
XX CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
XX CC culturing the host cell. (I) is also useful for targeting a polypeptide
XX CC of interest to a mitochondrial membrane, where ANT polypeptide is
XX CC expressed as a fusion protein with the polypeptide of interest.
XX CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
XX CC useful for identifying an agent that binds to an ANT polypeptide. ANT
XX CC ligand is useful for determining the presence of an ANT polypeptide,
XX CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
XX CC ANT from a biological sample, where the ANT ligand is covalently or non-
XX CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
XX CC useful for identifying an agent that interacts with an ANT polypeptide.
XX CC The present sequence represents the amino acid sequence of human ANT3.
XX SQ Sequence 298 AA;

Query Match 89.2%; Score 1385.5; DB 23; Length 298;
Best Local Similarity 87.2%; Pred. No. 1.5e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAWFLKDFLAGAATAVAVPIERVKLLQVQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQVHASKQIAADKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLAG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLAG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-AQRBFHGLGDCIIIFKSDGLRGILYQGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-AQRBFHGLGDCIIIFKSDGLRGILYQGFNVS 180
QY 180 VQGIILYRAAYFGYDTAKMLPDPKXNVHIFVSNMIAQSVTAVAGLLSYFPDTRRRMM 239
DB 181 VQGIILYRAAYFGYDTAKMLPDPKXNVHIFVSNMIAQSVTAVAGLLSYFPDTRRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIIFDEGKAPFKGAWSNVLRGMGAFVLVLYDLKKVY 297
DB 241 QSGRKGADIMYTGTVDCWRKIIFDEGKAPFKGAWSNVLRGMGAFVLVLYDLKKVY 298

RESULT 14
AAM41427
XX ID AAM41427 standard; Protein; 323 AA.
XX AC AAM41427;

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XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 6358.
XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX OS Homo sapiens.
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US34263.
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
XX DR N-PSDB; AAI60583.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries.
XX PS Example 2; SEQ ID NO 6358; 10078pp; English.
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification.
XX SQ Sequence 323 AA;

Query Match 89.2%; Score 1385.5; DB 22; Length 323;
Best Local Similarity 87.2%; Pred. No. 1.7e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAWFLKDFLAGAATAVAVPIERVKLLQVQVHASKQISAEKQYKGIIDCVVR 60
DB 26 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQVHASKQIAADKQYKGIIDCVVR 85
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLAG 120
DB 86 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLAG 145

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121 GAAGATSLCFVYPLDFAFTRLAADVRR-AQREPHGLGDCIIKIFKSDGLRGYQGFNVS 179  
146 GAAGATSLCFVYPLDFAFTRLAADVRR-AQREPHGLGDCIIKIFKSDGLRGYQGFNVS 205  
180 VQGIIRYRAAYFGVYDTAKGMLPDPKQVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 239  
206 VQGIIRYRAAYFGVYDTAKGMLPDPKQVHIFVSWMIAQSVTAVAGLLSYFPDTRRRMM 265  
240 QSGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYDEIKKV 297  
266 QSGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYDEIKKV 323

RESULT 15  
ABG15423  
ID ABG15423 standard; Protein; 325 AA.  
XX AC ABG15423;  
XX 18-FEB-2002 (first entry)  
XX Novel human diagnostic protein #15414.  
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US08631.  
XX 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
XX N-PSDB; AAS79610.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity  
XX Claim 20; SEQ ID No 45782; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 325 AA;  
Query Match 83.4%; Score 1294.5; DB 22; Length 325;  
Best Local Similarity 83.4%; Pred. No. 8e-143;  
Matches 251; Conservative 19; Mismatches 26; Indels 5; Gaps 4;  
Qy 1 MGDHWSFLKDFLAGAVAAVSKTAVAPTERVKLLQVOHASKQISAEKQYKGIIDCVVR 60  
Db 24 MTDAAVSFAKDFLAGVAAAISKTAVAPTERVKLLQVOHASKQIAADQYKGIIDCVVR 83  
Qy 61 IPKEQGFSLFWGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120  
Db 84 IPKEQGFSLFWGNLANVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 143  
Qy 121 GAAGATSLCFVYPLDFAFTRLAADVRR-AQREPHGLGDCIIKIFKSDGLRGYQGFNVS 179  
Db 144 GAAGATSLCFVYPLDFAFTRLAADVRR-AQREPHGLGDCIIKIFKSDGLRGYQGFNVS 203  
Qy 180 VQGIIRYRAAYFGVYDTAKGMLPDPKQVHIFVSWMIAQSV-TAVAGLLSYFPDTRRR 236  
Db 204 VQGIIRYRAAYFGVYDTAKGMLPDPKQVHIFVSWMIAQSV-TAVAGLLSYFPDTRRR 263  
Qy 237 MMQSGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYDEIKK 295  
Db 264 EXMQSGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYDEIKK 323  
Qy 296 Y 296  
Db 324 Y 324

Search completed: December 30, 2003, 09:55:59  
Job time : 43 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:53:51 ; Search time 21 Seconds  
(without alignments)  
1360.100 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 1553

Sequence: 1 MGDHAWSFUKFLAGVAAA.....LRMGGAFLVLYDEIKKTV 297

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526.5	98.3	298	1 A44778	ADP,ATP carrier pr
2	1466.5	94.4	298	2 I60173	adenine nucleotide
3	1463.5	94.2	298	2 S37210	ADP,ATP carrier pr
4	1458.5	93.9	298	1 XWBO	ADP,ATP carrier pr
5	1391.5	89.6	298	1 A29132	ADP,ATP carrier pr
6	1385.5	89.2	298	1 S03894	ADP,ATP carrier pr
7	1380.5	88.9	298	2 B43846	ADP,ATP carrier pr
8	1368.5	88.1	298	2 S31814	ADP,ATP carrier pr
9	1142.5	73.6	301	1 S31935	ADP,ATP carrier pr
10	1045.5	67.3	313	2 T25850	hypothetical prote
11	1043.5	67.2	313	2 T23207	hypothetical prote
12	1037.5	66.8	300	2 T25371	hypothetical prote
13	1005.5	64.7	300	2 T15206	hypothetical prote
14	973.5	62.7	339	2 A41677	ADP,ATP carrier pr
15	904.5	58.2	301	2 S51132	ADP,ATP carrier pr
16	772	49.7	306	2 T20012	hypothetical prote
17	770.5	49.6	308	1 S30259	ADP,ATP carrier pr
18	756.5	48.7	322	2 S14876	ADP,ATP carrier pr
19	752.5	48.5	332	2 T40526	ADP,ATP carrier pr
20	752.5	48.5	386	2 T09709	ADP,ATP carrier pr
21	751.5	48.4	387	2 S16568	ADP,ATP carrier pr
22	746.5	48.1	379	2 T04608	ADP,ATP carrier pr
23	746.5	48.1	382	2 S33630	ADP,ATP carrier pr
24	745.5	48.0	326	2 T25728	hypothetical prote
25	745.5	48.0	386	2 S17917	ADP,ATP carrier pr
26	744.5	47.9	386	2 S21974	ADP,ATP carrier pr
27	740	47.6	379	2 S21313	ADP,ATP carrier pr
28	740	47.6	386	2 S14874	ADP,ATP carrier pr
29	737	47.5	385	1 S29852	ADP,ATP carrier pr

30	736	47.4	307	2 A36582	ADP,ATP carrier pr
31	734	47.3	318	1 A31978	ADP,ATP carrier pr
32	733.5	47.2	313	1 XWNC	ADP,ATP carrier pr
33	729	46.9	305	2 S68154	ADP,ATP carrier pr
34	728.5	46.9	306	2 T42011	ADP,ATP carrier pr
35	718.5	46.3	309	2 A24849	ADP,ATP carrier pr
36	676	43.5	298	2 T24029	hypothetical prote
37	508	32.7	327	2 T51577	ADP/ATP translocas
38	368	23.7	415	2 T48171	hypothetical prote
39	367.5	23.7	325	2 T04273	hypothetical prote
40	363	23.4	381	2 T51158	hypothetical prote
41	350.5	22.6	475	2 T50686	peroxisomal Ca-dep
42	349.5	22.5	352	2 T01729	mitochondrial solu
43	345.5	22.2	358	2 T45934	hypothetical prote
44	334.5	21.5	348	2 D84798	probable mitochond
45	327	21.1	332	2 T47703	Ca-dependent solut

#### ALIGNMENTS

##### RESULT 1

A44778

ADP,ATP carrier protein T1 - human

N;Alternate names: mitochondrial ADP,ATP translocase 1

C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text\_change 17-Mar-2000

C:Accession: A44778; S03893; A39891; A28116

R:Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.;

J. Biol. Chem. 264, 13998-14004, 1989

A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located c

A:Reference number: A44778; MUID:89340499; PMID:2547778

A:Accession: A44778

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-298 <LIA>

A:Cross-references: GB:J04982; NID:g178658; PIDN:AAAS1736.1; PID:g178659

R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.

J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tra

A:Reference number: S03893; MUID:89236396; PMID:2541251

A:Accession: S03893

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <COZ>

R:Neckelmann, N.; Li, X.; Wade, R.P.; Shuster, R.; Wallace, D.C.

Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987

A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader

A:Reference number: A39891; MUID:88041149; PMID:2823266

A:Accession: A39891

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>

A:Cross-references: GB:J03966; NID:g339919; PIDN:AAAG1233.1; PID:g339920

A:Experimental source: clone pHMAT

R:Houldsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a c

A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: A28116

A:Molecule type: mRNA

A:Residues: 1-37 <HOU>

A:Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725

A:Experimental source: liver

C:Genetics:

A:Gene: GDB:ANT1; T1

A:Cross-references: GDB:119680; OMIM:103220

A:Map position: 4q35-q435

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

F;2-298/Product: ADP,ATP carrier protein #status predicted <MAT>

F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.3%; Score 1526.5; DB 1; Length 298;  
Best Local Similarity 98.3%; Pred. No. 1.5e-130; Indels 1; Gaps 1;  
Matches 293; Conservative 2; Mismatches 2;  
QY 1 MGDHWSFLKDFLAGAATAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
DB 1 MGDHWSFLKDFLAGGAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 180  
QY 180 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDTRRRMM 239  
DB 181 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDTRRRMM 240  
QY 240 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGGAFFVLVLYDEIKKYV 297  
DB 241 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGGAFFVLVLYDEIKKYV 298

## RESULT 2

160173  
adenine nucleotide translocator - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999  
C;Accession: I60173  
R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.  
Biochim. Biophys. Acta 1152, 192-196, 1993  
A;Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat  
A;Reference number: I60173; MUID:94002161; PMID:8399300  
A;Accession: I60173  
A;Status: preliminary; translated from GH/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-298 <RES>  
A;Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA43842.1; PID:9400427  
C;Genetics:  
A;Introns: 37/3; 200/1; 247/1  
A;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C;Keywords: duplication; transmembrane protein  
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>  
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.4%; Score 1466.5; DB 2; Length 298;  
Best Local Similarity 94.3%; Pred. No. 4.1e-125;  
Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;  
QY 1 MGDHWSFLKDFLAGAATAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
DB 1 MGDHWSFLKDFLAGGAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 180  
QY 180 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDTRRRMM 239  
DB 181 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDTRRRMM 240  
QY 240 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGGAFFVLVLYDEIKKYV 297

Db 241 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGGAFFVLVLYDEIKKYV 298

## RESULT 3

S37210  
ADP,ATP carrier protein T1 - mouse  
N;Alternate names: adenine nucleotide carrier  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Aug-1999  
C;Accession: S37210  
R;Laplace, C.; Costet, P.  
submitted to the EMBL Data Library, September 1993  
A;Reference number: S37210  
A;Accession: S37210  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-298 <LAP>  
A;Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628  
C;Genetics:  
A;Gene: ANCI  
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C;Keywords: duplication; transmembrane protein  
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>  
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

## Query Match

94.2%; Score 1463.5; DB 2; Length 298;  
Best Local Similarity 94.0%; Pred. No. 7.6e-125;  
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;  
QY 1 MGDHWSFLKDFLAGAATAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
DB 1 MGDHWSFLKDFLAGGAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 179  
DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 180  
QY 180 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDTRRRMM 239  
DB 181 VQGIIRYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAAGLLSYFPDTRRRMM 240  
QY 240 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGGAFFVLVLYDEIKKYV 297  
DB 241 QSGRKGADIMYTGTCVDCWRKIADKDEGAKAFKFGAWSNVLRGMGGAFFVLVLYDEIKKYV 298

## RESULT 4

XWBO  
ADP,ATP carrier protein T1 - bovine  
N;Alternate names: ADP/ATP translocase T1  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 14-Nov-1983 #sequence\_revision 22-Jul-1994 #text\_change 22-Jun-1999  
C;Accession: A43646; A24822; A03181; A61343; S69369  
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.  
Biochemistry 28, 866-873, 1989  
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in  
A;Reference number: A43646; MUID:89229093; PMID:2540808  
A;Accession: A43646  
A;Molecule type: mRNA  
A;Residues: 1-298 <POM>  
A;Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415  
R;Rasmussen, U.B.; Wohlrab, H.  
Biochem. Biophys. Res. Commun. 138, 850-857, 1986  
A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual  
A;Reference number: A24822; MUID:86295775; PMID:3017341  
A;Accession: A24822  
A;Molecule type: mRNA  
A;Residues: 208-298 <RAS>

A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631  
 R;Aquila, H.; Migra, D.; Eulitz, M.; Klingenberg, M.  
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982  
 A;Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria  
 A;Reference number: A03181; MUID:82198267; PMID:7076130  
 A;Accession: A03181  
 A;Molecule type: protein  
 A;Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AQ>  
 A;Note: residue 52 may be methyllysine  
 R;Babel, W.; Wächter, E.; Aquila, H.; Klingenberg, M.  
 Biochim. Biophys. Acta 670, 176-180, 1981  
 A;Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria  
 A;Reference number: A61343; MUID:82046808; PMID:62711240  
 A;Accession: A61343  
 A;Molecule type: protein  
 A;Residues: 205-298 <BAB>  
 R;Oettmeier, W.; Masson, K.; Kalinna, S.  
 Eur. J. Biochem. 227, 730-733, 1995  
 A;Title: [(3H)7-azido-4-isobutyryl]acridone labels Cyel59 of the bovine mitochondrial ADP/ATP carrier  
 A;Reference number: S69369; MUID:95172058; PMID:7867632  
 A;Accession: S69369  
 A;Molecule type: protein  
 A;Residues: 49-63;154-168 <OET>  
 C;Comment: This protein is synthesized in the cytosol and transported into the mitochondria  
 C;Complex: homodimer  
 C;Function:  
 A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP  
 A;Note: located in the inner mitochondrial membrane  
 C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
 C;Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitochondria  
 F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>  
 F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>  
 F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>  
 F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental  
 F;52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 93.9%; Score 1458.5; DB 1; Length 298;  
 Best Local Similarity 94.3%; Pred. No. 2.2e-124;  
 Matches 281; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGAAVAVSTAVPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60  
 DB 1 MSDQALSFLKDFLAGGVAIAISKTAVPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60

QY 61 IPKEQGLSFWRGNLNANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLAG 120  
 DB 61 IPKEQGLSFWRGNLNANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLAG 120

QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 179  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 180

QY 180 VQGIILYRAAYFGYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRMM 239  
 DB 180 VQGIILYRAAYFGYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRMM 240

QY 240 QSGRKADIMYTGTVDCWRKIADGKAPFKGANSNVLKGMGSAFVLVLYDEIKYV 297  
 DB 241 QSGRKADIMYTGTVDCWRKIADGKAPFKGANSNVLKGMGSAFVLVLYDEIKYV 298

RESULT 5  
 A29132  
 ADP/ATP carrier protein T2 - human  
 N;Alternate names: mitochondrial ADP/ATP translocase 2  
 C;Species: Homo sapiens (man)  
 C;Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
 C;Accession: A29132; C28116  
 R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.  
 J. Biol. Chem. 262, 4355-4359, 1987  
 A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated  
 A;Reference number: A29132; MUID:87166056; PMID:3031073  
 A;Accession: A29132

A;Molecule type: mRNA  
 A;Residues: 1-298 <BAT>  
 A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247  
 R;Houldsworth, J.; Attardi, G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
 A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
 A;Reference number: A94197; MUID:88124845; PMID:2829183  
 A;Accession: C28116  
 A;Molecule type: mRNA  
 A;Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>  
 A;Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721  
 A;Experimental source: clone PHAT3  
 C;Genetics:  
 A;Gene: GDB:ANT2; T3; 2F1  
 A;Cross-references: GDB:125190; OMIM:300150  
 A;Map position: Xq13-Qx26  
 A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:ANT1  
 C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
 C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>  
 F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>  
 F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 89.6%; Score 1391.5; DB 1; Length 298;  
 Best Local Similarity 88.6%; Pred. No. 2.5e-118;  
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGAAVAVSTAVPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60  
 DB 1 MTDALSPAFKDFLAGGVAIAISKTAVPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60

QY 61 IPKEQGLSFWRGNLNANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLAG 120  
 DB 61 IPKEQGLSFWRGNLNANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLAG 120

QY 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 179  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGR-RAQREPHGLGDCIIKIFKSDGLRGLYQGFNVS 180

QY 180 VQGIILYRAAYFGYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRMM 239  
 DB 180 VQGIILYRAAYFGYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRMM 240

QY 240 QSGRKADIMYTGTVDCWRKIADGKAPFKGANSNVLKGMGSAFVLVLYDEIKYV 296  
 DB 241 QSGRKADIMYTGTVDCWRKIADGKAPFKGANSNVLKGMGSAFVLVLYDEIKYV 297

RESULT 6  
 S03894  
 ADP/ATP carrier protein T3 - human  
 N;Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP/ATP  
 C;Species: Homo sapiens (man)  
 C;Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
 C;Accession: S03894; B28116  
 R;Cozens, A.L.; Runswick, M.J.; Walker, J.E.  
 J. Mol. Biol. 206, 261-280, 1989  
 A;Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr  
 A;Reference number: S03893; MUID:89236396; PMID:2541251  
 A;Accession: S03894  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-298 <COZ>  
 R;Houldsworth, J.; Attardi, G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
 A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
 A;Reference number: A94197; MUID:88124845; PMID:2829183  
 A;Accession: B28116  
 A;Molecule type: mRNA  
 A;Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>  
 A;Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723  
 A;Experimental source: liver  
 C;Genetics:



F:112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F:209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 73.6%; Score 1142.5; DB 1; Length 301;  
Best Local Similarity 76.2%; Pred. No. 8.8e-96;  
Matches 221; Conservative 26; Mismatches 42; Indels 1; Gaps 1;  
QY 6 WSLKDFLAGAATAAASKTAVAPIERVKLLQVQHASQKISAEKQYKGIIDCVVRIPEQ 65  
DB 8 YGPAKDFLAGGISAASKTAVAPIERVKLLQVQHASQKISAEKQYKGIIDCVVRIPEQ 67  
QY 66 GFLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDHKKQFWRYPAGNLASGGAAGA 125  
DB 68 GIGAFCCGNLANVIRYPTQALNFAKDKYKQLFLGGVDHKKQFWRYPAGNLASGGAAGA 127  
QY 126 TSCFVYPLDFAFTRLAADVGRRA-OREFHGLGDCIIKIPKSDGLRGLYOGFNVSQGI 184  
DB 128 TSCFVYPLDFAFTRLAADVGRRA-OREFHGLGDCIIKIPKSDGLRGLYOGFNVSQGI 187  
QY 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPTDTRRRMMQSGRK 244  
DB 188 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPTDTRRRMMQSGRK 247  
QY 245 GADIMYTGTVDCWRKIADKDEGAKAFKPGAMSNVLRGMGAFVLVLYDEIK 294  
DB 248 KSEVMYKNTLDCVAKIKCKQSGGAFKPGAMSNVLRGMGAFVLVLYDEIK 297

## RESULT 10

T25850  
hypothetical protein T01B11.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000  
R:Geisel, C.; Stellyes, L.  
submitted to the EMBL Data Library, December 1996  
A:Description: The sequence of C. elegans cosmid T01B11.  
A:Reference number: Z20099  
A:Accession: T25850  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-313 <GFI>  
A:Cross-references: EMBL:U80931; PIDN:AA838001.1; GSPDB:GN00022; CESP:T01B11.4  
A:Experimental source: strain Bristol N2; clone T01B11  
C:Genetics:  
A:Gene: CESP:T01B11.4  
A:Map position: 4  
A:Introns: 4/1; 191/2  
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1045.5; DB 2; Length 313;  
Best Local Similarity 69.8%; Pred. No. 5.6e-87;  
Matches 203; Conservative 36; Mismatches 49; Indels 3; Gaps 2;  
QY 8 FLKDFLAGAATAAASKTAVAPIERVKLLQVQHASQKISAEKQYKGIIDCVVRIPEQ 67  
DB 25 FLIDLASGGTAAASKTAVAPIERVKLLQVQHASQKISAEKQYKGIIDCVVRIPEQ 84  
QY 68 LSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDHKKQFWRYPAGNLASGGAAGA 127  
DB 85 AALWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDHKKQFWRYPAGNLASGGAAGA 144  
QY 128 LCFVYPLDFAFTRLAADVGRRA-OREFHGLGDCIIKIPKSDGLRGLYOGFNVSQGI 187  
DB 145 LCFVYPLDFAFTRLAADVGRRA-OREFHGLGDCIIKIPKSDGLRGLYOGFNVSQGI 204  
QY 188 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPTDTRRRMMQSGRK 246  
DB 205 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPTDTRRRMMQSGRK 262  
QY 247 DIMYTGTVDCWRKIADKDEGAKAFKPGAMSNVLRGMGAFVLVLYDEIK 297  
DB 263 DVLYKNTLDCVAKIKCKQSGGAFKPGAMSNVLRGMGAFVLVLYDEIK 313

## RESULT 11

T23207  
hypothetical protein K01H12.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000  
C:Accession: T23207  
R:McMurray, A.  
submitted to the EMBL Data Library, December 1995  
A:Reference number: Z19707  
A:Accession: T23207  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-313 <WIL>  
A:Cross-references: EMBL:Z68218; PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.2  
A:Experimental source: clone K01H12  
C:Genetics:  
A:Gene: CESP:K01H12.2  
A:Map position: 4  
A:Introns: 4/1; 191/2  
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.2%; Score 1043.5; DB 2; Length 313;  
Best Local Similarity 69.4%; Pred. No. 8.5e-87;  
Matches 202; Conservative 37; Mismatches 49; Indels 3; Gaps 2;  
QY 8 FLKDFLAGAATAAASKTAVAPIERVKLLQVQHASQKISAEKQYKGIIDCVVRIPEQ 67  
DB 25 FLIDLASGGTAAASKTAVAPIERVKLLQVQHASQKISAEKQYKGIIDCVVRIPEQ 84  
QY 68 LSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDHKKQFWRYPAGNLASGGAAGA 127  
DB 85 AALWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDHKKQFWRYPAGNLASGGAAGA 144  
QY 128 LCFVYPLDFAFTRLAADVGRRA-OREFHGLGDCIIKIPKSDGLRGLYOGFNVSQGI 187  
DB 145 LCFVYPLDFAFTRLAADVGRRA-OREFHGLGDCIIKIPKSDGLRGLYOGFNVSQGI 204  
QY 188 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPTDTRRRMMQSGRK 246  
DB 205 AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPTDTRRRMMQSGRK 262  
QY 247 DIMYTGTVDCWRKIADKDEGAKAFKPGAMSNVLRGMGAFVLVLYDEIK 297  
DB 263 DVLYKNTLDCVAKIKCKQSGGAFKPGAMSNVLRGMGAFVLVLYDEIK 313

## RESULT 12

T25371  
hypothetical protein T27E9.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000  
C:Accession: T25371  
R:Lloyd, C.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z20024  
A:Accession: T25371  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-300 <WIL>  
A:Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021; CESP:T27E9.1  
A:Experimental source: clone T27E9  
C:Genetics:  
A:Gene: CESP:T27E9.1  
A:Map position: 3  
A:Introns: 20/1; 41/3; 115/2  
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 66.8%; Score 1037.5; DB 2; Length 300;  
Best Local Similarity 69.1%; Pred. No. 2.8e-86;  
Matches 201; Conservative 38; Mismatches 49; Indels 3; Gaps 2;

Qy	8	FLKDFLAGAAAVSKTAVAP	IERVKLLQVQVHASKQISAEKQVKGII	CDVWRIPKEQGF	67
Db	12	FLTDLASGGTAAAVSKTAVAP	IERVKLLQVQDASKAIAVDKRYKGM	IMLVIRVPKEQV	71
Qy	68	LSEWRGNLANVIRYPTQALNFA	PKDKYKQJFLGGVDNRHKOFRYFAGN	LASGGAAGATS	127
Db	72	AALWRGNLANVIRYPTQAMNFA	PKDTYKAIFLEGDKKDFWKFPFAGN	LASGGAAGATS	131
Qy	128	LCFVYPLDPARTLAAADVGRRA	QREFFHGLGDCIITIKFSGDLRGLY	QGFNVVSGIIIVR	187
Db	132	LCFVYPLDPARTLAAADIGKAND	REFKGLADCLIKIVKSDGPIGLYR	GFFVSGIIIVR	191
Qy	188	AAVFGVYDTAKGML--PDPKNVHI	FYSVMIAQSVTAAGLLSYDPDTR	VRRRMMQSGRKA	246
Db	192	AAVFGMFDIAKGVFASDGQKLN	FFAAWGIAQVTVTGGSLISYPM	DTVRRRMMQSGRK--	249
Qy	247	DIMYGTVDVCRKIAKDEGA	KAFPKGAWSNLVRGMGGAFLV	LYDEIKCYV	297
Db	250	DILYKNLTDCAKKIIQNEGMS	AMPFGALSNVFRGTGGALV	LAIDEYDETKEL	300

RESULT 13  
T15206  
hypothetical protein W02D3.6 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jan-2000  
C:Accession: T15206  
R:Le, T.; Weinstock, L.; Rifkin, L.  
submitted to the EMBL Data Library, May 1997  
A:Description: The sequence of *C. elegans* cosmid W02D3.  
A:Reference number: Z18308  
A:Accession: T15206  
A:Status: preliminary; translated from GE/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-300 <LEFT>  
A:Cross-references: EMBL:AF003141; NID:G2088732; PID:G2088738; PIDN:ARB54179.1; GSPDB:GN  
A:Experimental source: strain Bristol N2; Clone W02D3  
C:Genetics:  
A:Gene: CESP:W02D3.6  
A:Map position: 1  
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
F:9-103/Domain: ADP, ATP carrier protein repeat homology <ACR>

Query Match	64.7%;	Score 1005.5;	DB 2;	Length 300;
Best Local Similarity	66.0%;	Pred. No. 2.2e-83;		
Matches 192;	Conservative 40;	Mismatches 56;	Indels 3;	Gaps 2
QY	8	FLKDFLAGVAANAASKTAVATIERVKLLQLQVHASKOISAEKQYKGIHDCVVRIPKEQGF	67	
DB	12	FLVLDLASGGTAAAIKSTAVATIERVKLLQVDSYSETVTADKKYKGMIDVLARVPKEQGY	71	
QY	68	LSFWRGNLANVIRYPTQALNPAFKDKYQKFLGCGVDRHKQFWRYFAGNINLASGGAAGATS	127	
DB	72	AAFWRGNLANVIRYPTQALNPAFKDITYKMFQEGIDKNKEFWKFFAGNINLASGGAAGATS	131	
QY	128	LCFVYPLDFPARTRLAADVGRRAQREFHGLGDCIITIKFKSDGLKGLYQGFNVSVQGIHII	187	
DB	132	LCFVYPLDFVTRRLGADVKGWDREFQGLTDCFKVIKSDGPTGLYRGFPVSVQGIHII	191	
QY	188	AAAYFGYDTAKGML-PDPKNVHI FVSMWIAQSVTAVAGLLSYFPDVTVRMMMQSGRKA	246	
DB	192	AAAYFGMEDTAKLYSTDGQKLNFFTTWAI AQVGTGVSGLSYSPWDVTVRMMMQSGRK--	249	
QY	247	DIWYTGTVDCWRKIAKDGAKAAPFKGAWSNVLRGMGGAFLVILYDEIKKYV	297	
DB	250	DILYKNTLDCVRKIVKNSGIIATLYKGLSNVFRATGCAVLITYDEIHLI	300	

RESULT 14  
A41677  
ADP,ATP carrier protein - Chlorella kessleri  
C:Species: Chlorella kessleri  
C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 20-Aug-1999

C:Accession: A41677  
 R: Hilgarth, C.; Sauer, N.; Tanner, W.  
 J. Biol. Chem. 266, 24044-24047, 1991  
 A: Title: Glucose increases the expression of the ATP/ADP translocator and the glyceralde-  
 A: Reference number: A41677; MUID: P2084708; PMID: 1748677  
 A: Accession: A41677  
 A: Status: preliminary  
 A: Molecule type: mRNA  
 A: Residues: 1-339 <HL>  
 A: Cross-references: GB:M76669; NID:G516596; PIDN:AAA33027.1; PID:G516597  
 C: Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C: Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F: 38-134/Domain: ADP, ATP carrier protein repeat homology <ACPI>  
 F: 144-235/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
 F: 241-329/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match	62.7%;	Score	973.5;	DB	2;	Length	339;
Best Local Similarity	65.3%;	Pred. No.	2e-80;				
Matches	192;	Conservative	30;	Mismatches	65;	Indels	7;
						Gaps	4;
Qy	7	SFLKDLFLAGAAVAASKTAVAPIERVKLLIQVHASKQISAEK--QYKGIIIDCVVRIPKE	64				
Db	40	AFVKDLLAGGTAGIAKSTAVAPIERVKLLLTQDSNPMIKSGQVPRTGTGVNCFVRSVS	99				
Qy	65	QGFLSPWRGNLANVIRYFPTQALNFAKDKYKQLFLGGVDRHKQWRYFAGNHLASGGAG	124				
Db	100	QGVASFWRGNLANVIRYFPTQAFNFAKDTIKGLF-PKYSPTKDFWRFVFNVLASGGLAG	158				
Qy	125	ATSLCFVYPLDFARTLAAADVGRRAOREFHGLGDCI IKIFKSDGLRGLYQGFGNVSVQGII	184				
Db	159	AGSLLIVYPLDFARTLAAADVVGSGKSRFTGLVLDCLSKVVKRGGPMALYQGFVGSVOGII	218				
Qy	185	IYFAAYFGVYDTAKGML-PDPKNVHIVFSWMIAQSVTAVAGLISYFDDTVRRMMQSGR	243				
Db	219	VIYGAIFGLYDTAKGVLFKDDRTANFPAKWAQAQVATAGVLSYFDDTVRRKLMQSG--	276				
Qy	244	KGADIMYTGTVDCWRKXIAKDEGAKAPFKGAWSNVLRGMGGAFLVLVIYDIKXYV	297				
Db	277	-GGEROYNGTIDCWRKVAOEGMKAPFKGAWSNVLRGAGGAFLVLVIYDIKIKFI	329				

RESULT 15  
S51132  
ADP.ATP carrier protein - malaria parasite (Plasmodium falciparum)  
N/Alternate names: ADP/ATP transporter  
C/Species: Plasmodium falciparum  
C/Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jun-2000  
C/Accession: S68993, S51132  
R/Hatin, I.; Jaureguiberry, G.  
Eur. J. Biochem. 228, 86-91, 1995  
A/Title: Molecular characterisation of the ADP/ATP-transporter cDNA from the  
A/Reference number: S68993; MUID:95188918; PMID:7883016  
A/Accession: S68993  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-301 <HAT>  
A/Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335  
C/Superfamily: ADP.ATP carrier protein; ADP.ATP carrier protein repeat homo  
C/Keywords: duplication; transmembrane protein  
F/6-102/Domain: ADP.ATP carrier protein repeat homology <ACPI>  
F/119-203/Domain: ADP.ATP carrier protein repeat homology <ACP2>  
F/209-301/Domain: ADP.ATP carrier protein repeat homology <ACP3>

	Query Match	58.2%	Score 904.5	DB 2	Length 301
	Best Local Similarity	58.3%	Pred. No. 3.1e-74		
	Matches 172	Conservative 48	Mismatches 70	Indels 5	Gaps 4
Qy	7	SLFKDFLAGA <del>AA</del> AVKSTAVAPIERVKLLQLVQHASKQISA--EKQYKGIIDCVVRIPKE	64		
Db	8	NFAADFAMGGISAASKVTVTPIERVKMLIQDSEIPEIKSQQVERYSGLINCFRRVSKSE	67		
Qy	65	QGFPLSWRGNLANVIRYPTPTALNFAFKDKYKQLFLGGVDHRHKQWRYEPAGNLAGSGAAG	124		



Db 68 QGVLSLWRGNVANVIRYFPTQAFNFAFYKYNIP-PRYDQNTDFSKFFCVNLSGATAG 126  
QY 125 ATSLCFVYPLDPARTLAAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYOGFNVSVQGI 184  
Db 127 AISLLIYPLDPARTLRLASDYGKDRQFTGLFDCLAKYKQTGLLSLYSGFGVSVTGI 186  
QY 185 IYRAAYFGVYDTAKGML-PDPKNVHIFVSMIAQSVTAVAGLLSYPPDTRRRMMMSGR 243  
Db 187 VYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVAQSVTILAGLISYPPDTRRRMMMSGR 246  
QY 244 KG-ADIMYTGTVDCWKRKIAKDEGAKAFKGANVLRGMGGAFVLVLYDEIKYV 297  
Db 247 KGKEIOYKNTIDCWIKILRNEGKGFPGAWANVIRGAGGALVLVYDELOKLI 301

Search completed: December 30, 2003, 09:57:26  
Job time : 22 secs

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